

SEQUENCE LISTING

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 Watkins, Maren
 Olivera, Baldomero M.

<120> B-Superfamily Conotoxins

<130> 2314-248

<150> US 60/264323

<151> 2001-01-29

<160> 340

<170> PatentIn version 3.0

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 Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg
 15 20 25 30

ggt ttg gtg cca gat gac tta acc cca cag ctt att ttg caa agt ctg 144
 Gly Leu Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Gln Ser Leu
 35 40 45

gat tcc cgt cgt cat gat cac ggc att cgt ccg aag aga gtc gac ata 192
 Asp Ser Arg Arg His Asp His Gly Ile Arg Pro Lys Arg Val Asp Ile
 50 55 60

tgt aac tgg agg ata tgt gca cca aac cca ttg aga cga cat gat ctt 240
 Cys Asn Trp Arg Ile Cys Ala Pro Asn Pro Leu Arg Arg His Asp Leu
 65 70 75

aag aaa gga aac aat tgacgtcaga caaccgccac aacttgagta cgacatcggt 295
 Lys Lys Gly Asn Asn
 80

aatacgactt cagcaaatat gaaattttca gcatcactgt gggtgtgaag aaatcagttg 355

ctttaaaagg ttggatttgt ccttggttaa gccgttgtac tgatgacatc tctgcactat 415

gaaataaagc tgatgtgaca aactaaaaaa aaaaaaaaaa a 456

<210> 2
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 <213> Conus flavidus

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 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30
 Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Gln Ser Leu Asp Ser
 35 40 45
 Arg Arg His Asp His Gly Ile Arg Pro Lys Arg Val Asp Ile Cys Asn
 50 55 60
 Trp Arg Ile Cys Ala Pro Asn Pro Leu Arg Arg His Asp Leu Lys Lys
 65 70 75 80

Gly Asn Asn

<210> 3
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 <213> Conus flavidus
 <220>
 <221> PEPTIDE
 <222> (1)..(33)
 <223> Xaa at residues 7, 20 and 22 may be Pro or hydroxy-Pro; Xaa at re
 sidue 15 may be Trp (Dor L) or bromo-Trp (Dor L)

<400> 3
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 1 5 10 15
 Ile Cys Ala Xaa Asn Xaa Leu Arg Arg His Asp Leu Lys Lys Gly Asn
 20 25 30

Asn

<210> 4
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 <213> Conus miles

<220>
 <221> CDS
 <222> (7)..(315)

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 1 5 10
 ggg ctc acc gtc ggg agt cac gtc cat cgg tct cac agt cct aca tcg 96
 Gly Leu Thr Val Gly Ser His Val His Arg Ser His Ser Pro Thr Ser
 15 20 25 30
 cgc agc cat ggt gat gac tcc att cat gac aag acg att cat caa cat 144
 Arg Ser His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His
 35 40 45
 ctg ttt gcc cgt ctt cct ctg gag aac aac gac gac cat cgt tct gtg 192
 Leu Phe Ala Arg Leu Pro Leu Glu Asn Asn Asp Asp His Arg Ser Val
 50 55 60

agt cct cat cat gtg tgt tgt gct att ggt ccg gtt ctt cca ttc tgt 288
 Ser Pro His His Val Cys Cys Ala Ile Gly Pro Val Leu Pro Phe Cys
 80 85 90

actcaggaat agacagaaag gcaaaaaaaaaa aaaaaaaaaa . 374

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<400> 5
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Gly Leu
1          5          10          15
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His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His Leu Phe
35 40 45

Pro Ala Gly Asn Gly Ala Gly Asn Thr Lys Gln Gln Asp Gln Ser Pro
65 70 75 80

Ser Trp Leu His Lys Leu His
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<220>
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<222> (1)..(29)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residues 6, 15 and 18
may be Pro or hydroxy-Pro; Xaa at residue 24 may be Trp (D or L)
or bromo-Trp (D or L)
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Leu Cys Phe Cys Cys Val Ser Xaa Leu His Lys Leu His
20 25

<210>	7
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<213> Conus miles

<220>

<221> CDS

<222> (7)..(291)

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1 5 10

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Gly Phe Thr Val Gly Gly His Val His Arg Ser His Ser Pro Thr Ser
15 20 25 30

cgc agc cat ggt gat gac tcc att cat gac aag acg att cat caa cat 144
Arg Ser His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His
35 40 45

ctg ttt gcc cgt ctt cct cag gag aac aac gac gac cat cgt tct gtg 192
Leu Phe Ala Arg Leu Pro Gln Glu Asn Asn Asp Asp His Arg Ser Val
50 55 60

gat ctt cct gca ggg act agc gca ggc gac atg aaa cca caa cgc caa 240
Asp Leu Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln
65 70 75

aga cgt ctc tgc tgc atc ttt gcc ccg att ctt tgg ttc tgt tgt cac 288
Arg Arg Leu Cys Cys Ile Phe Ala Pro Ile Leu Trp Phe Cys Cys His
80 85 90

ggt taacagctca aattacactg cactggccga ttgaaagaac tgcaataaac 341
Gly
95

ggaaaaaaaa aaaaaaaaaa 359

<210> 8

<211> 95

<212> PRT

<213> Conus miles

<400> 8

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Gly Phe
1 5 10 15

Thr Val Gly Gly His Val His Arg Ser His Ser Pro Thr Ser Arg Ser
20 25 30

His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His Leu Phe
35 40 45

Ala Arg Leu Pro Gln Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu
50 55 60

Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln Arg Arg
65 70 75 80

Leu Cys Cys Ile Phe Ala Pro Ile Leu Trp Phe Cys Cys His Gly
85 90 95

<210> 9

<211> 14

<212> PRT

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<213> Conus miles

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Xaa at residue 7 may be Pro or hydroxy-Pro; Xaa at residue 10 may be Trp (D or L) or bromo-Trp (D or L)

<400> 9

Leu Cys Cys Ile Phe Ala Xaa Ile Leu Xaa Phe Cys Cys His
1 5 10

<210> 10

<211> 351

<212> DNA

<213> Conus capitaneus

<220>

<221> CDS

<222> (7)..(291)

<400> 10

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1 5 10

ggg ttc acc gtc ggg ggt cac gtc cat cgg tct cac agt cct aca tcg 96
Gly Phe Thr Val Gly Gly His Val His Arg Ser His Ser Pro Thr Ser
15 20 25 30

cgc agc cat ggt gat gac tcc att cat gac gag acg att cat caa cat 144
Arg Ser His Gly Asp Asp Ser Ile His Asp Glu Thr Ile His Gln His
35 40 45

ctg ttt gcc cgt ctt cct cag gag aac aac gac gac cat cgt tct gtg 192
Leu Phe Ala Arg Leu Pro Gln Glu Asn Asn Asp Asp His Arg Ser Val
50 55 60

gat ctt cct gca ggg act agc gca ggc gac atg aaa cca caa cgc caa 240
Asp Leu Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln
65 70 75

aga ggt ttc tgc tgc gac ttt ccc ccg att ttt tgg ttc tgt tgt atc 288
Arg Gly Phe Cys Cys Asp Phe Pro Pro Ile Phe Trp Phe Cys Cys Ile
80 85 90

ggt taacagcaca aattacactg cactggccga ttgaaagaac tgcaataaac 341
Gly

95
ggaaaaaaaaa 351

<210> 11

<211> 95

<212> PRT

<213> Conus capitaneus

<400> 11

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Gly Phe
1 5 10 15

Thr Val Gly Gly His Val His Arg Ser His Ser Pro Thr Ser Arg Ser
20 25 30

His Gly Asp Asp Ser Ile His Asp Glu Thr Ile His Gln His Leu Phe

20250606 16:03:33

35 40 45

Ala Arg Leu Pro Gln Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu
50 55 60

Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln Arg Gly
65 70 75 80

Phe Cys Cys Asp Phe Pro Pro Ile Phe Trp Phe Cys Cys Ile Gly
85 90 95

<210> 12
<211> 15
<212> PRT
<213> *Conus capitaneus*

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residues 7 and 8 may be Pro or hydroxy-Pro; Xaa at residue
11 may be Trp (D or L) or bromo-Trp (D or L)

<400> 12
Gly Phe Cys Cys Asp Phe Xaa Xaa Ile Phe Xaa Phe Cys Cys Ile
1 5 10 15

<210> 13
<211> 348
<212> DNA
<213> *Conus generalis*

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<221> CDS
<222> (7)..(222)

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1 5 10

att aaa ggc cct gtg tct gaa ggt ggt aaa ttg aac gac gta att cgg 96
Ile Lys Gly Pro Val Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg
15 20 25 30

ggt ttg gtg cca gac gac ttg acc cca gtg ttt gcc ttg cat cat ccg 144
Gly Leu Val Pro Asp Asp Leu Thr Pro Val Phe Ala Leu His His Pro
35 40 45

gtt tcc cat cgt cgg tct cac agc agt agt ttg tgg tgt gta tgt cca 192
Val Ser His Arg Arg Ser His Ser Ser Ser Leu Trp Cys Val Cys Pro
50 55 60

ttc agg gtg tgt cca cca tgc cat gga aga tgacctggtc ccaaaccaac 242
Phe Arg Val Cys Pro Pro Cys His Gly Arg
65 70

aaaataacgt cagacaaccg ccacaacttt agtacgacat cccttaatac gacttcagca 302
agtatttttaa catcactatg gtgtgatgaa atcagttgct ttaaaa 348

<210> 14
<211> 72
<212> PRT
<213> *Conus generalis*

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 20 25 30
 Val Pro Asp Asp Leu Thr Pro Val Phe Ala Leu His His Pro Val Ser
 35 40 45
 His Arg Arg Ser His Ser Ser Ser Leu Trp Cys Val Cys Pro Phe Arg
 50 55 60
 Val Cys Pro Pro Cys His Gly Arg
 65 70

<210> 15
 <211> 19
 <212> PRT
 <213> Conus generalis
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 <221> PEPTIDE
 <222> (1)..(19)
 <223> Xaa at residue 7 may be Trp (D or L) or bromo-Trp (D or L); Xaa a
 t residues 11, 16 and 17 may be Pro or hydroxy-Pro

<400> 15
 Ser His Ser Ser Ser Leu Xaa Cys Val Cys Xaa Phe Arg Val Cys Xaa
 1 5 10 15

Xaa Cys His

<210> 16
 <211> 405
 <212> DNA
 <213> Conus wittigi

<220>
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 <222> (1)..(210)
 <220>
 <221> misc_feature
 <222> (1)..(405)
 <223> n may be any base

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 1 5 10 15
 aag cac gta att cgg ggt ttg gtg cca gac gac tta acc cca cag ctt 96
 Lys His Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Pro Gln Leu 20 25 30
 20 25 30
 atc ttg cga agt ctg att tcc cgt cgt agt tct gac ggc agt gat ccg 144
 Ile Leu Arg Ser Leu Ile Ser Arg Arg Ser Ser Asp Gly Ser Asp Pro 35 40 45
 35 40 45
 aag gca aaa aaa cag tgt atg tgg aag aga tgt ata cca gac caa tcg 192
 Lys Ala Lys Lys Gln Cys Met Trp Lys Arg Cys Ile Pro Asp Gln Ser 50 55 60
 50 55 60

aga cta gaa gaa gat gaa tgaatgacaga caaccgccat cactgtagta 240
 Arg Leu Glu Glu Asp Glu
 65 70

tgacatcggtt aatacgactt aagcaaatat ttttaacatca ctgtgggttct gaagacatca 300

gttgcttttaa aagattggat tcttccttgt ttaagagttg tactganatc attcctgccc 360

tgtgaaataa agctgatggtt gacanncaaa caaaaaaaaa aaaaa 405

<210> 17

<211> 70

<212> PRT

<213> Conus wittigi

<400> 17

Met Met Leu Val Trp Ile Thr Ala Pro Leu Pro Glu Gly Gly Lys Leu
 1 5 10 15

Lys His Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Pro Gln Leu
 20 25 30

Ile Leu Arg Ser Leu Ile Ser Arg Arg Ser Ser Asp Gly Ser Asp Pro
 35 40 45

Lys Ala Lys Lys Gln Cys Met Trp Lys Arg Cys Ile Pro Asp Gln Ser
 50 55 60

Arg Leu Glu Glu Asp Glu
 65 70

<210> 18

<211> 29

<212> PRT

<213> Conus wittigi

<220>

<221> PEPTIDE

<222> (1)..(29)

<223> Xaa at residues 7 and 20 may be Pro or hydroxy-Pro; Xaa at residue 15 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 26, 27 and 29 may be Glu or Glu

<400> 18

Ser Ser Asp Gly Ser Asp Xaa Lys Ala Lys Lys Gln Cys Met Xaa Lys
 1 5 10 15

Arg Cys Ile Xaa Asp Gln Ser Arg Leu Xaa Xaa Asp Xaa
 20 25

<210> 19

<211> 463

<212> DNA

<213> Conus consors

<220>

<221> CDS

<222> (7)..(222)

<400> 19

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 1 5 10

att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att cgg 96
 Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg
 15 20 25 30

ggt ttg gtg tca cac atc tta atc cca cag cat acc ttg cga agt ctg 144
 Gly Leu Val Ser His Ile Leu Ile Pro Gln His Thr Leu Arg Ser Leu
 35 40 45

act tcc cgt gat cgt tct gac aac ggt ggt tcg agt gga gca caa ata 192
 Thr Ser Arg Asp Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile
 50 55 60

tgc atc tgg aag gta tgt cca cca tcc cca tagagacgac cacgaggaaa 242
 Cys Ile Trp Lys Val Cys Pro Pro Ser Pro
 65 70

aagatgaacg gcgtcagaca accgccacaa ctgtagtacg acatcgttga tacgacttca 302
 gcaactatatt taacatcact gtggttgtga agaaatcagt cgctttaaaa gattggattt 362
 ttccttgttt aagagttgta ctgatatcag ctctgcacta tgaaataaag ctgatgtgac 422
 ataaaaaaaa aaaaaaaaaag tactctgcgt tgttactcga g 463

<210> 20
 <211> 72
 <212> PRT
 <213> Conus consors

<400> 20
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 1 5 10 15
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30
 Val Ser His Ile Leu Ile Pro Gln His Thr Leu Arg Ser Leu Thr Ser
 35 40 45
 Arg Asp Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile
 50 55 60
 Trp Lys Val Cys Pro Pro Ser Pro
 65 70

<210> 21
 <211> 23
 <212> PRT
 <213> Conus consors

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 16 may be Trp (D or L) or bromo-Trp (D or L); Xaa
 at residues 20, 21 and 23 may be Pro or hydroxy-Pro

<400> 21
 Asp Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Xaa
 1 5 10 15
 Lys Val Cys Xaa Xaa Ser Xaa
 20

<210> 22
 <211> 470
 <212> DNA
 <213> Conus consors

<220>
 <221> CDS
 <222> (7)..(246)

<400> 22
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 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp
 1 5 10
 att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gca att cgg 96
 Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Ala Ile Arg
 15 20 25 30
 ggt ttg gtg tca cac atc tta atc cca cag cat acc ttg cga agt ctg 144
 Gly Leu Val Ser His Ile Leu Ile Pro Gln His Thr Leu Arg Ser Leu
 35 40 45
 act tcc cgt gct cgt tct gac aac ggt ggt tcg agt gga gca caa ata 192
 Thr Ser Arg Ala Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile
 50 55 60
 tgc atc tgg aag gta tgt cca cca tcc cca tgg aga cga cca caa gga 240
 Cys Ile Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Pro Gln Gly
 65 70 75
 aaa aga tgaatgacgt cagacaaccg ccacaactgt agtacgacat cggttgatacg 296
 Lys Arg
 80
 acttcagcaa atattttaac atcactgtgg ttgtgaagaa atcagttgct ttaaaagatt 356
 ggattttttcc ttgtttaaga gttgtactga tatcagctct gcactatgaa ataaagctga 416
 tgtgacaaac aataaaaaag aaaaaaaaaa aagtactctg cggttggtact cgag 470

<210> 23
 <211> 80
 <212> PRT
 <213> Conus consors

<400> 23
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 1 5 10 15
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Ala Ile Arg Gly Leu
 20 25 30
 Val Ser His Ile Leu Ile Pro Gln His Thr Leu Arg Ser Leu Thr Ser
 35 40 45
 Arg Ala Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile
 50 55 60
 Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Pro Gln Gly Lys Arg
 65 70 75 80

<210> 24
 <211> 28
 <212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residues 16 and 24 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 20, 21, 23 and 27 may be Pro or hydroxy-Pro

<400> 24

Ala Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Xaa
1 5 10 15

Lys Val Cys Xaa Xaa Ser Xaa Xaa Arg Arg Xaa Gln
20 25

<210> 25

<211> 469

<212> DNA

<213> Conus consors

<220>

<221> CDS

<222> (7)..(228)

<400> 25

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1 5 10

att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att cgg 96
Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg
15 20 25 30

ggt ttg gtg cca cac ttc tta acc cca cag cat atc ttg caa agt ctg 144
Gly Leu Val Pro His Phe Leu Thr Pro Gln His Ile Leu Gln Ser Leu
35 40 45

act tcc cgt aat ggt tct ggc agc agt aat cag aaa gaa gca caa cta 192
Thr Ser Arg Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu Ala Gln Leu
50 55 60

tgc atc tgg aag gta tgt cca cca tcc cca tgg aga tgaccacaag 238
Cys Ile Trp Lys Val Cys Pro Pro Ser Pro Trp Arg
65 70

gaaaaagatg aacggcgtca gacaaccgcc acaactgtag tgggacatcg ttgatacgac 298

ttcagcaaatt attttaacat cactgtgggt gtgaagaaat cagttgcttt aaaagattgg 358

atTTTTcctt gTTtaagaat tGtactgata tCagctctgc actatgaaat aaagctgatg 418

tGacaaccca aaaaaaaaaa aaaaaaaaaag tactctgcg__tgttactcga g 469

<210> 26

<211> 74

<212> PRT

<213> Conus consors

<400> 26

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
20 25 30

205210 4693504

Val Pro His Phe Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser
35 40 45

Arg Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu Ala Gln Leu Cys Ile
50 55 60

Trp Lys Val Cys Pro Pro Ser Pro Trp Arg
65 70

<210> 27

<211> 25

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 10 may be Glu or Gla; Xaa at residues 16 and 24 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 20, 21 and 23 may be Pro or hydroxy-Pro

<400> 27

Asn Gly Ser Gly Ser Ser Asn Gln Lys Xaa Ala Gln Leu Cys Ile Xaa
1 5 10 15

Lys Val Cys Xaa Xaa Ser Xaa Xaa Arg
20 25

<210> 28

<211> 472

<212> DNA

<213> Conus tulipa

<220>

<221> CDS

<222> (7)..(231)

<220>

<221> misc_feature

<222> (1)..(472)

<223> n may be any base

<400> 28

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Met Gln Thr Ala Tyr Trp Val Met Leu Met Met Met Val Trp
1 5 10

att aca gcc cct ctg tct gaa ggt ggt aaa ctg aac gac gta att cgg 96
Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg
15 20 25 30

ggt ttg gtg cca cac gtc tta acc cca cag cat atc ttg caa agt ctg 144
Gly Leu Val Pro His Val Leu Thr Pro Gln His Ile Leu Gln Ser Leu
35 40 45

gtt tcc cgt cgt cat ttt aac agc gtt gtt ccg acg gta tac ata tgc 192
Val Ser Arg Arg His Phe Asn Ser Val Val Pro Thr Val Tyr Ile Cys
50 55 60

atg tgg aag gta tgt cca cca tcg cca tag aga cga cca taaggaaaa 241
Met Trp Lys Val Cys Pro Pro Ser Pro Arg Arg Pro
65 70

gatgaatgac gtcagacaac cgccacaact gtagtacgac atcggttaata cgacttcagc 301

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aaatatttta acatcactgt ggttgtgaag aaatcagttg ctttaaaaga ttggattttt 361
 ccttgtttca gagttgtact gatatacagct ctgcactatc aaataaagct gaagtgacaa 421
 accnnaaaaa aaaaaaaaaa aaaaaaaag tactctgcgt tggttactcga g 472

<210> 29
 <211> 71
 <212> PRT
 <213> Conus tulipa

<400> 29
 Met Gln Thr Ala Tyr Trp Val Met Leu Met Met Met Val Trp Ile Thr
 1 5 10 15
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30
 Val Pro His Val Leu Thr Pro Gln His Ile Leu Gln Ser Leu Val Ser
 35 40 45
 Arg Arg His Phe Asn Ser Val Val Pro Thr Val Tyr Ile Cys Met Trp
 50 55 60
 Lys Val Cys Pro Pro Ser Pro
 65 70

<210> 30
 <211> 21
 <212> PRT
 <213> Conus tulipa

<220>
 <221> PEPTIDE
 <222> (1)..(21)
 <223> Xaa at residues 7, 18, 19 and 21 may be Pro or hydroxy-Pro; Xaa at
 residue 10 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-
 sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Trp or brom
 o-Trp

<400> 30
 His Phe Asn Ser Val Val Xaa Thr Val Xaa Ile Cys Met Xaa Lys Val
 1 5 10 15
 Cys Xaa Xaa Ser Xaa
 20

<210> 31
 <211> 451
 <212> DNA
 <213> Conus tulipa

<220>
 <221> CDS
 <222> (1)..(279)

<400> 31
 atg cag acg gcc tac tgg gtg atg ctg ttg atg atg gtg ggc att aca 48
 Met Gln Thr Ala Tyr Trp Val Met Leu Leu Met Met Val Gly Ile Thr
 1 5 10 15
 gcc cct ctg cct gaa ggt ggt aaa ccg aac agc gta att cgg ggt ttg 96
 Ala Pro Leu Pro Glu Gly Gly Lys Pro Asn Ser Val Ile Arg Gly Leu

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20 25 30

gtg cca aac gac tta act cca cag cat acc ttg cga agt ctg att tcc 144
Val Pro Asn Asp Leu Thr Pro Gln His Thr Leu Arg Ser Leu Ile Ser
35 40 45

cgt cgt caa act gac gtt ctt ctg gag gct acc ctt ttg aca aca cca 192
Arg Arg Gln Thr Asp Val Leu Leu Glu Ala Thr Leu Leu Thr Thr Pro
50 55 60

gcc ccc gag cag aga ttg ttc tgc ttc tgg aag tca tgt tgg cca agg 240
Ala Pro Glu Gln Arg Leu Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg
65 70 75 80

ccc tac cct tgg aga cga cgt gat ctt aat gga aaa cga tgaatgacgt 289
Pro Tyr Pro Trp Arg Arg Arg Asp Leu Asn Gly Lys Arg
85 90

cagacaaccg ccacaactgt agtacgacat cattaatacgc acttcagcaa atattttaac 349

attactgtgg ttgtgaagaa atcacttgct ttaaaagatt ggttttttcc ttgtttcaga 409

gttgactga tatcagctct gccctatgaa ataaagctga tg 451

<210> 32
<211> 93
<212> PRT
<213> Conus tulipa

<400> 32
Met Gln Thr Ala Tyr Trp Val Met Leu Leu Met Met Val Gly Ile Thr
1 5 10 15

Ala Pro Leu Pro Glu Gly Gly Lys Pro Asn Ser Val Ile Arg Gly Leu
20 25 30

Val Pro Asn Asp Leu Thr Pro Gln His Thr Leu Arg Ser Leu Ile Ser
35 40 45

Arg Arg Gln Thr Asp Val Leu Leu Glu Ala Thr Leu Leu Thr Thr Pro
50 55 60

Ala Pro Glu Gln Arg Leu Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg
65 70 75 80

Pro Tyr Pro Trp Arg Arg Arg Asp Leu Asn Gly Lys Arg
85 90

<210> 33
<211> 40
<212> PRT
<213> Conus tulipa

<220>
<221> PEPTIDE
<222> (1)..(40)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 7 and 17 may
be Glu or Gla; Xaa at residue 14, 16, 29, 31 and 33 may be Pro or
hydroxy-Pro; Xaa at residues 24, 28 and 34 may be Trp (D or L) o
r bromo-Trp (D or L)

<220>
<221> PEPTIDE
<222> (1)..(40)

<223> Xaa at residue 32 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 33

Xaa Thr Asp Val Leu Leu Xaa Ala Thr Leu Leu Thr Thr Xaa Ala Xaa
1 5 10 15

Xaa Gln Arg Leu Phe Cys Phe Xaa Lys Ser Cys Xaa Xaa Arg Xaa Xaa
20 25 30

Xaa Xaa Arg Arg Arg Asp Leu Asn
35 40

<210> 34

<211> 414

<212> DNA

<213> Conus sulcatus

<220>

<221> CDS

<222> (1)..(285)

<400> 34

atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
1 5 10 15

gcc cct ctg tct gaa ggt ggt aaa ccg aac gac gta att cgg ggt ttg 96
Ala Pro Leu Ser Glu Gly Gly Lys Pro Asn Asp Val Ile Arg Gly Leu
20 25 30

gtg cca gac gac tta acc cca cag cgt gtc ttg cga agt ctg att tcc 144
Val Pro Asp Asp Leu Thr Pro Gln Arg Val Leu Arg Ser Leu Ile Ser
35 40 45

cgt cgt caa tct ggc tgc aga gtc ccg ttt gaa ttg aaa tgc atc tgg 192
Arg Arg Gln Ser Gly Cys Arg Val Pro Phe Glu Leu Lys Cys Ile Trp
50 55 60

aag ttc tgt aca ata tac cca tcg aga cca ttt gct tct ctg gaa gaa 240
Lys Phe Cys Thr Ile Tyr Pro Ser Arg Pro Phe Ala Ser Leu Glu Glu
65 70 75 80

aaa gac gaa tgt cag aca gtc acc ata act gta aca tgg gat ttt 285
Lys Asp Glu Cys Gln Thr Val Thr Ile Thr Val Thr Trp Asp Phe
85 90 95

taatacgtct ccagcaagta ttttaacatc actgtggttg tgaagaaatc agttgcttta 345

aaagattgga tttttccttg ttttaagagtt gtactgatat cagctctgcc ctgtgaaata 405

aagctgatg 414

<210> 35

<211> 95

<212> PRT

<213> Conus sulcatus

<400> 35

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Pro Asn Asp Val Ile Arg Gly Leu
20 25 30

Val Pro Asp Asp Leu Thr Pro Gln Arg Val Leu Arg Ser Leu Ile Ser
35 40 45

Arg Arg Gln Ser Gly Cys Arg Val Pro Phe Glu Leu Lys Cys Ile Trp
50 55 60

Lys Phe Cys Thr Ile Tyr Pro Ser Arg Pro Phe Ala Ser Leu Glu Glu
65 70 75 80

Lys Asp Glu Cys Gln Thr Val Thr Ile Thr Val Thr Trp Asp Phe
85 90 95

<210> 36

<211> 45

<212> PRT

<213> Conus sulcatus

<220>

<221> PEPTIDE

<222> (1)..(45)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residues 7, 21 and 24 may be Pro or hydroxy-Pro; Xaa at residues 9, 29, 30 and 33 may be Glu or Gla; Xaa at residues 14 and 43 may be Trp (D or L) or bromo-Trp (D or L)

<220>

<221> PEPTIDE

<222> (1)..(45)

<223> Xaa at residue 20 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 36

Xaa Ser Gly Cys Arg Val Xaa Phe Xaa Leu Lys Cys Ile Xaa Lys Phe
1 5 10 15

Cys Thr Ile Xaa Xaa Ser Arg Ser Phe Ala Ser Leu Xaa Xaa Lys Asp
20 25 30

Xaa Cys Gln Thr Val Thr Ile Thr Val Thr Xaa Asp Phe
35 40 45

<210> 37

<211> 413

<212> DNA

<213> Conus sulcatus

<220>

<221> CDS

<222> (1)..(234)

<400> 37

atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
1 5 10 15

gcc tct ctg tct gaa ggt ggt aaa ccg aac gac gtc att cgg ggt ttt 96
Ala Ser Leu Ser Glu Gly Gly Lys Pro Asn Asp Val Ile Arg Gly Phe
20 25 30

gtg cca gac gac tta acc cca cag ctt atc ttg cga agt ctg att tcc 144
Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Arg Ser Leu Ile Ser
35 40 45

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cgt cgt cgt tct gac aag gat gtt ggg aag aga atg gaa tgt tac tgg 192
 Arg Arg Arg Ser Asp Lys Asp Val Gly Lys Arg Met Glu Cys Tyr Trp
 50 55 60

aag gca tgt aga ccc acg cta tcg aga cga cat gat ctt ggg 234
 Lys Ala Cys Arg Pro Thr Leu Ser Arg Arg His Asp Leu Gly
 65 70 75

taaaagatga atgacgtcag acaacagcca caactatagt atgacatcgt taatacgact 294

tcagcaaata ttttaacatc actgtgggtg tgaagaaatc agttgcttta aaagattgga 354

tttttcctgtg ttttaagagtt gtactgatat cagctctgcc ctgtgaaata aagctgatg 413
 <210> 38
 <211> 78
 <212> PRT
 <213> Conus sulcatus

<400> 38
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Val Trp Ile Thr
 1 5 10 15

Ala Ser Leu Ser Glu Gly Gly Lys Pro Asn Asp Val Ile Arg Gly Phe
 20 25 30

Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Arg Ser Leu Ile Ser
 35 40 45

Arg Arg Arg Ser Asp Lys Asp Val Gly Lys Arg Met Glu Cys Tyr Trp
 50 55 60

Lys Ala Cys Arg Pro Thr Leu Ser Arg Arg His Asp Leu Gly
 65 70 75

<210> 39
 <211> 27
 <212> PRT
 <213> Conus sulcatus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 11 may be Glu or Gla; Xaa at residue 13 may be Pro
 or hydroxy-Pro; Xaa at residue 14 may be Trp (D or L) or bromo-T
 rp (D or L); Xaa at residue 19 may be Tyr, 125I-Tyr, mono-iodo-Ty
 r, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 39
 Arg Ser Asp Lys Asp Val Gly Lys Arg Met Xaa Cys Xaa Xaa Lys Ala
 1 5 10 15

Cys Arg Xaa Thr Leu Ser Arg Arg His Asp Leu
 20 25

<210> 40
 <211> 451
 <212> DNA
 <213> Conus magus

<220>
 <221> CDS
 <222> (1)..(279)

<400> 40

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atg cag acg gcc tac tgg gtg atg ctg atg atg atg gtg tgc atc aca      48
Met Gln Thr Ala Tyr Trp Val Met Leu Met Met Met Val Cys Ile Thr
1          5          10

gcc cct ctg cct gaa ggt ggt aaa ccg aac agc gga att cgg ggt ttg      96
Ala Pro Leu Pro Glu Gly Gly Lys Pro Asn Ser Gly Ile Arg Gly Leu
          20          25          30

gtg cca aac gac tta act cca cag cat acc ttg cga agt ctg att tcc      144
Val Pro Asn Asp Leu Thr Pro Gln His Thr Leu Arg Ser Leu Ile Ser
          35          40          45

cgt cgt caa act gac gtt ctt ctg gat gct acc ctt ttg aca aca cca      192
Arg Arg Gln Thr Asp Val Leu Leu Asp Ala Thr Leu Leu Thr Thr Pro
          50          55          60

gcc ccc gag cag aga ttg ttc tgc ttc tgg aag tca tgt tgg cca agg      240
Ala Pro Glu Gln Arg Leu Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg
65          70          75          80

ccc tac cct tgg aga cga cgt aat ctt aat gga aaa cga tgaatgacgt      289
Pro Tyr Pro Trp Arg Arg Arg Asn Leu Asn Gly Lys Arg
          85          90

cagacaaccg ccacaactgt agtacgacat cgттаатacg acttcagcaa atattttaac      349

ataactgtgg ttgtgaagaa atcggttgct ttaaaagatt ggatttttcc ttgtttcaga      409

gttgactga tatgagctct gccctgtgaa ataaagctga tg                        451

<210> 41
<211> 93
<212> PRT
<213> Conus magus

<400> 41
Met Gln Thr Ala Tyr Trp Val Met Leu Met Met Met Val Cys Ile Thr
1          5          10

Ala Pro Leu Pro Glu Gly Gly Lys Pro Asn Ser Gly Ile Arg Gly Leu
          20          25          30

Val Pro Asn Asp Leu Thr Pro Gln His Thr Leu Arg Ser Leu Ile Ser
          35          40          45

Arg Arg Gln Thr Asp Val Leu Leu Asp Ala Thr Leu Leu Thr Thr Pro
          50          55          60

Ala Pro Glu Gln Arg Leu Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg
65          70          75          80

Pro Tyr Pro Trp Arg Arg Arg Asn Leu Asn Gly Lys Arg
          85          90

<210> 42
<211> 40
<212> PRT
<213> Conus magus

<220>
<221> PEPTIDE
<222> (1)..(40)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residues 14, 16, 29,
31 and 33 may be Pro or hydroxy-Pro; Xaa at residue 17 may be Glu

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or Glu; Xaa at residues 24, 28 and 34 may be Trp (D or L) or bromo-Trp (D or L)

<220>
 <221> PEPTIDE
 <222> (1)..(40)
 <223> Xaa at residue 32 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 42
 Xaa Thr Asp Val Leu Leu Asp Ala Thr Leu Leu Thr Thr Xaa Ala Xaa
 1 5 10 15

Xaa Gln Arg Leu Phe Cys Phe Xaa Lys Ser Cys Xaa Xaa Arg Xaa Xaa
 20 25 30

Xaa Xaa Arg Arg Arg Asn Leu Asn
 35 40

<210> 43
 <211> 423
 <212> DNA
 <213> Conus emaciatus

<220>
 <221> CDS
 <222> (1)..(249)

<400> 43
 atg cag acg gcc tac tgg gtg atg gcg atg atg atg gtg tgg att aca 48
 Met Gln Thr Ala Tyr Trp Val Met Ala Met Met Met Val Trp Ile Thr
 1 5 10 15

gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att cgg ggt ttg 96
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30

gtg cca gat gac tta acc cca cag ctt gtt ttg caa agt ctg gat tcc 144
 Val Pro Asp Asp Leu Thr Pro Gln Leu Val Leu Gln Ser Leu Asp Ser
 35 40 45

cgt cgt cat act cac ggc att cgt ccg aag gga gac ggc ata tgt atc 192
 Arg Arg His Thr His Gly Ile Arg Pro Lys Gly Asp Gly Ile Cys Ile
 50 55 60

tgg aag gta tgt cca cca gac cca tgg aga cga cat cgt ctt aag aaa 240
 Trp Lys Val Cys Pro Pro Asp Pro Trp Arg Arg His Arg Leu Lys Lys
 65 70 75 80

aga aac aat tgacgtcaga caaccgccac aacttgagta cgacatcggt 289
 Arg Asn Asn

aatacagactt cagcaaatat gaaattttca gcatcactgt gggtgtcaag aaatcagttg 349

ctttaaaaga ttggatttgt ccttggtttaa gagttgtact gatgtcagct ctgccctgtg 409

aaataaagct gatg 423

<210> 44
 <211> 83
 <212> PRT
 <213> Conus emaciatus

Conus emaciatus

<400> 44
 Met Gln Thr Ala Tyr Trp Val Met Ala Met Met Met Val Trp Ile Thr
 1 5 10 15
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30
 Val Pro Asp Asp Leu Thr Pro Gln Leu Val Leu Gln Ser Leu Asp Ser
 35 40 45
 Arg Arg His Thr His Gly Ile Arg Pro Lys Gly Asp Gly Ile Cys Ile
 50 55 60
 Trp Lys Val Cys Pro Pro Asp Pro Trp Arg Arg His Arg Leu Lys Lys
 65 70 75 80

Arg Asn Asn

<210> 45
 <211> 33
 <212> PRT
 <213> Conus emaciatus
 <220>
 <221> PEPTIDE
 <222> (1)..(33)
 <223> Xaa at residues 7, 19, 20 and 22 may be Pro or hydroxy-Pro; Xaa at
 residues 15 and 23 may be Trp (D or L) or bromo-Trp (D or L)

<400> 45
 His Thr His Gly Ile Arg Xaa Lys Gly Asp Gly Ile Cys Ile Xaa Lys
 1 5 10 15
 Val Cys Xaa Xaa Asp Xaa Xaa Arg Arg His Arg Leu Lys Lys Arg Asn
 20 25 30

Asn

<210> 46
 <211> 412
 <212> DNA
 <213> Conus circumciscus

<220>
 <221> CDS
 <222> (1)..(240)

<400> 46
 atg cag acg gcc tac tgg gtg atg gtg atg atg gtg gtg tgg att aca 48
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Val Val Trp Ile Thr 15
 1 5 10
 gcc cct ctg tct gaa ggt ggt aaa tcg aac gac gta att cgg ggt ttg 96
 Ala Pro Leu Ser Glu Gly Gly Lys Ser Asn Asp Val Ile Arg Gly Leu 20 25 30
 gtg cca cac atc tta acc cca cag cat atc ttg caa agt ctg act tcc 144
 Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser 35 40 45
 cgt ctt cgt tct gac agc agt ggt cag aaa gga gca caa ata tgc atc 192
 Arg Leu Arg Ser Asp Ser Ser Gly Gln Lys Gly Ala Gln Ile Cys Ile 50 55 60

tgg aag gta tgt cca cta tcc cca tgg aga cga cca caa gga aaa aga 240
 Trp Lys Val Cys Pro Leu Ser Pro Trp Arg Arg Pro Gln Gly Lys Arg
 65 70 75 80

tgaatgacgt cagacaaccg ctacaactgt agtacgacat cgttgatacg acttcagcaa 300

atattttaac atcactgtgg ttgtgaagaa atcagttgct ttaaaagatt ggatttttcc 360

ttgtttaaga gttgtactga tatcagctct gccctgtgaa ataaagctga tg 412

<210> 47

<211> 80

<212> PRT

<213> Conus circumcisis

<400> 47

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Val Val Trp Ile Thr
 1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Ser Asn Asp Val Ile Arg Gly Leu
 20 25 30

Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser
 35 40 45

Arg Leu Arg Ser Asp Ser Ser Gly Gln Lys Gly Ala Gln Ile Cys Ile
 50 55 60

Trp Lys Val Cys Pro Leu Ser Pro Trp Arg Arg Pro Gln Gly Lys Arg
 65 70 75 80

<210> 48

<211> 28

<212> PRT

<213> Conus circumcisis

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residues 16 and 24 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 20, 23 and 27 may be Pro or hydroxy-Pro

<400> 48

Leu Arg Ser Asp Ser Ser Gly Gln Lys Gly Ala Gln Ile Cys Ile Xaa
 1 5 10 15

Lys Val Cys Xaa Leu Ser Xaa Xaa Arg Arg Xaa Gln
 20 25

<210> 49

<211> 410

<212> DNA

<213> Conus betulinus

<220>

<221> CDS

<222> (1)..(207)

<400> 49

atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
 1 5 10 15

gcc cct ctg tcc gaa ggt ggt aaa ctg aac gat gta att cgg gct ttg 96
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Ala Leu

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20              25              30
gcg cca gac gac gta acc cca cag ttt atc ttg cga agt ctg att tcc      144
Ala Pro Asp Asp Val Thr Pro Gln Phe Ile Leu Arg Ser Leu Ile Ser
      35              40              45

cgt cgt cgt tct gac agc gat gtt cgg gag gta ccc gta tgt tcc tgg      192
Arg Arg Arg Ser Asp Ser Asp Val Arg Glu Val Pro Val Cys Ser Trp
      50              55              60

aag ata tgt cca cca tagccataga gacgacatga tcttaaggaa aaagagaaat      247
Lys Ile Cys Pro Pro
65

gacgtcagac aaccgccaca actgtagtac ggcatcgtaa atacgacttc agcaaagtgt      307
ttaacatcac tgtgtgtgtg aagaaatcag ctgctttaaa agattggatt tttccttaag      367
agttgcactg atgtcagttc tgccctgtga aataaagctg atg      410

<210> 50
<211> 69
<212> PRT
<213> Conus betulinus

<400> 50
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
1              5              10              15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Ala Leu
      20              25              30

Ala Pro Asp Asp Val Thr Pro Gln Phe Ile Leu Arg Ser Leu Ile Ser
      35              40              45

Arg Arg Arg Ser Asp Ser Asp Val Arg Glu Val Pro Val Cys Ser Trp
      50              55              60

Lys Ile Cys Pro Pro
65

<210> 51
<211> 19
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (1)..(19)
<223> Xaa at residue 8 may be Glu or Gla; Xaa at residues 10, 18 and 19
      may be Pro or hydroxy-Pro; Xaa at residue 14 may be Trp (D or L)
      or bromo-Trp (D or L)

<400> 51
Arg Ser Asp Ser Asp Val Arg Xaa Val Xaa Val Cys Ser Xaa Lys Ile
1              5              10              15

Cys Xaa Xaa

<210> 52
<211> 423
<212> DNA
<213> Conus aurisiacus

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<220>
 <221> CDS
 <222> (1)..(249)

 <400> 52
 atg cag acg gcc tac tgg gtg atg gcg atg atg atg gtg tgg att aca 48
 Met Gln Thr Ala Tyr Trp Val Met Ala Met Met Met Val Trp Ile Thr
 1 5 10 15

 gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att cgg ggt ttg 96
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30

 gtg cca gat gac tta acc cca cag ctt gtt ttg caa agt ctg gat tcc 144
 Val Pro Asp Asp Leu Thr Pro Gln Leu Val Leu Gln Ser Leu Asp Ser
 35 40 45

 cgt cgt cat act cac ggc att cgt ccg aag gga gac ggc ata tgt atc 192
 Arg Arg His Thr His Gly Ile Arg Pro Lys Gly Asp Gly Ile Cys Ile
 50 55 60

 tgg aag gta tgt cca cca gac cca tgg aga cga cat cat ctt aag aaa 240
 Trp Lys Val Cys Pro Pro Asp Pro Trp Arg Arg His His Leu Lys Lys
 65 70 75 80

 aga aac aat tgacgtcaga caaccgccac aacttgagta cgacatcggt 289
 Arg Asn Asn

 aatacgaactt cagcaaatat gaaattttca gcatcactgt gggtgtcaag aaatcagttg 349
 ctttaaaaga ttggatttgt ccttggtttaa gagttgtact gatgtcagct ctgccctatg 409
 aaataaagct gatg 423

 <210> 53
 <211> 83
 <212> PRT
 <213> Conus aurisiacus

 <400> 53
 Met Gln Thr Ala Tyr Trp Val Met Ala Met Met Met Val Trp Ile Thr
 1 5 10 15

 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30

 Val Pro Asp Asp Leu Thr Pro Gln Leu Val Leu Gln Ser Leu Asp Ser
 35 40 45

 Arg Arg His Thr His Gly Ile Arg Pro Lys Gly Asp Gly Ile Cys Ile
 50 55 60

 Trp Lys Val Cys Pro Pro Asp Pro Trp Arg Arg His His Leu Lys Lys
 65 70 75 80

 Arg Asn Asn

 <210> 54
 <211> 33
 <212> PRT
 <213> Conus aurisiacus

<220>
 <221> PEPTIDE
 <222> (1)..(33)
 <223> Xaa at residues 7, 19, 20 and 22 may be Pro or hydroxy-Pro; Xaa at residues 1 and 24 may be Trp (D or L) or bromo-Trp (D or L)

<400> 54
 His Thr His Gly Ile Arg Xaa Lys Gly Asp Gly Ile Cys Ile Xaa Lys
 1 5 10 15
 Val Cys Xaa Xaa Asp Xaa Xaa Arg Arg His His Leu Lys Lys Arg Asn
 20 25 30

Asn

<210> 55
 <211> 439
 <212> DNA
 <213> Conus aurisiacus

<220>
 <221> CDS
 <222> (1)..(249)
 <400> 55
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
 1 5 10 15
 gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att tgg ggt ttg 96
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Trp Gly Leu
 20 25 30
 gtg cca cac atc tta acc cca cag cat atc ttg caa agc ctg act tcc 144
 Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser
 35 40 45
 cgt ctt cat tct gac agc agt gat cag aaa gga ggc atg aac gca tgg 192
 Arg Leu His Ser Asp Ser Ser Asp Gln Lys Gly Gly Met Asn Ala Trp
 50 55 60
 aca gga gca gga gca caa ata tgc atc tgg aag gta tgt cca cca ccc 240
 Thr Gly Ala Gly Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Pro
 65 70 75 80
 cca tgg aga tgaacacaag gaaaaagatg aatgacgtca gacaaccgcc 289
 Pro Trp Arg
 acaactgtag tacgacatcg ttgatacgac ttcagcaaatt attttaacat cactgtgggtt 349
 gtgaagaaat cagttgcttt aaaagattgg atttttcctt gtttaagagt tgtactgata 409
 tcagctctgc cctgtgaagt aaagctgatg 439

<210> 56
 <211> 83
 <212> PRT
 <213> Conus aurisiacus

<400> 56
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
 1 5 10 15

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Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Trp Gly Leu
 20 25 30
 Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser
 35 40 45
 Arg Leu His Ser Asp Ser Ser Asp Gln Lys Gly Gly Met Asn Ala Trp
 50 55 60
 Thr Gly Ala Gly Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Pro
 65 70 75 80
 Pro Trp Arg

<210> 57
 <211> 34
 <212> PRT
 <213> Conus aurisiacus

<220>
 <221> PEPTIDE
 <222> (1)..(34)
 <223> Xaa at residues 15, 25 and 33 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 29, 30, 31 and 32 may be Pro or hydroxy-Pro

<400> 57
 Leu His Ser Asp Ser Ser Asp Gln Lys Gly Gly Met Asn Ala Xaa Thr
 1 5 10 15
 Gly Ala Gly Ala Gln Ile Cys Ile Xaa Lys Val Cys Xaa Xaa Xaa Xaa
 20 25 30

Xaa Arg

<210> 58
 <211> 412
 <212> DNA
 <213> Conus aurisiacus

<220>
 <221> CDS
 <222> (1)..(222)

<400> 58
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Val Trp Ile Thr
 1 5 10 15
 gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att tgg ggt ttg 96
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Trp Gly Leu
 20 25 30
 gtg cca cac atc tta acc cca cag cat atc ttg caa agc ctg act tcc 144
 Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser
 35 40 45
 cgt ctt cat tct gac agc agt gat cag aaa gga gca caa ata tgc atc 192
 Arg Leu His Ser Asp Ser Ser Asp Gln Lys Gly Ala Gln Ile Cys Ile
 50 55 60
 tgg aag gta tgt cca cca ccc cca tgg aga tgaacacaag gaaaaagatg 242
 Trp Lys Val Cys Pro Pro Pro Pro Trp Arg

```
<210> 59
<211> 74
<212> PRT
<213> Conus aurisiacus
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```
<210> 60
<211> 25
<212> PRT
<213> Conus aurisiacus
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<400> 60
Leu His Ser Asp Ser Ser Asp Gln Lys Gly Ala Gln Ile Cys Ile Xaa
1          5          10          15
Lys Val Cys Xaa Xaa Xaa Xaa Arg
          20          25

```

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<220>
<221> CDS
<222> (1) .. (267)
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<400>      61
atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca          48
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
1              5                  10                15

gcc cct ctg ttt gaa ggt ggt aaa ttg aac gac gta att cgg ggt ttg          96
Ala Pro Leu Phe Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
                20                    25                30
```

gtg cca cac atc tta acc cca cag cat atc ttg caa agc ctg act tcc 144
Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser
35 40 45

cgt ctt cgt tct gac agc agt gat cag aaa gga ggc atg aac gca tcg 192
Arg Leu Arg Ser Asp Ser Ser Asp Gln Lys Gly Gly Met Asn Ala Ser
50 55 60

aca gga gca gga gca caa ata tgc atc tgg aag gta tgt cca cca tcc 240
Thr Gly Ala Gly Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Ser
65 70 75 80

cca tgg aga cga aca caa gga aaa aga tgaatgacgt cagacaaccg 287
Pro Trp Arg Arg Thr Gln Gly Lys Arg
85

ccacaactgt agtacgacat cgttgatacg acttcagcaa atattttaac atcactgtgg 347

ttgtgaagaa atcagttgct ttaaaagatt ggatttttcc ttgtttaaga gttgtactga 407

tatcagctct gcactgtgaa ataaagctga tg 439

<210> 62

<211> 89

<212> PRT

<213> Conus aurisiacus

<400> 62

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
1 5 10 15

Ala Pro Leu Phe Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
20 25 30

Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser
35 40 45

Arg Leu Arg Ser Asp Ser Ser Asp Gln Lys Gly Gly Met Asn Ala Ser
50 55 60

Thr Gly Ala Gly Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Ser
65 70 75 80

Pro Trp Arg Arg Thr Gln Gly Lys Arg
85

<210> 63

<211> 37

<212> PRT

<213> Conus aurisiacus

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residues 25 and 33 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 29, 30 and 32 may be Pro or hydroxy-Pro

<400> 63

Leu Arg Ser Asp Ser Ser Asp Gln Lys Gly Gly Met Asn Ala Ser Thr
1 5 10 15

Gly Ala Gly Ala Gln Ile Cys Ile Xaa Lys Val Cys Xaa Xaa Ser Xaa
20 25 30

$\langle 210 \rangle$	66
$\langle 211 \rangle$	28
$\langle 212 \rangle$	PRT

<213> *Conus achatinus*

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residues 16 and 24 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 20, 21, 23 and 27 may be Pro or hydroxy-Pro

<400> 66

Leu Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Xaa
1 5 10 15

Lys Val Cys Xaa Xaa Ser Xaa Xaa Arg Arg Xaa Gln
20 25

<210> 67

<211> 399

<212> DNA

<213> *Conus purpurascens*

<220>

<221> CDS

<222> (1)..(213)

<400> 67

atg cag acg gcc tac tgg gtg atg gtg atg acg atg gtg tgg att aca 48
Met Gln Thr Ala Tyr Trp Val Met Val Met Thr Met Val Trp Ile Thr
1 5 10 15

gcc cct ctg tct gaa ggt gga aaa ctg aac gat gta att cgg ggt ttg 96
Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
20 25 30

gtg cca gac gac tta gcc cta cag ctt atc ttg caa agt ccg gtt ttc 144
Val Pro Asp Asp Leu Ala Leu Gln Leu Ile Leu Gln Ser Pro Val Phe
35 40 45

cgt cgt caa tct gaa gag gaa aaa ata tgc ctc tgg aag ata tgt cca 192
Arg Arg Gln Ser Glu Glu Lys Ile Cys Leu Trp Lys Ile Cys Pro
50 55 60

cca ccc cca tgg aga cga tca taaggaaaaaaa aaaatgaatg acgtcagaca 243
Pro Pro Pro Trp Arg Arg Ser
65 70

accaccacaa ctgtaatacgt acatcggttaa tacgacttca gcaaacattt taacatcact 303

gtgggttgta agaaatcagt tgcttttagaa gcttggattt ttccttgttt aagagttgta 363

ctgatatcag ctctgcccta tgaaataaag ctgatg 399

<210> 68

<211> 71

<212> PRT

<213> *Conus purpurascens*

<400> 68

Met Gln Thr Ala Tyr Trp Val Met Val Met Thr Met Val Trp Ile Thr
1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
20 25 30

Val Pro Asp Asp Leu Ala Leu Gln Leu Ile Leu Gln Ser Pro Val Phe

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35 40 45
 Arg Arg Gln Ser Glu Glu Glu Lys Ile Cys Leu Trp Lys Ile Cys Pro
 50 55 60

 Pro Pro Pro Trp Arg Arg Ser
 65 70

 <210> 69
 <211> 21
 <212> PRT
 <213> Conus purpurascens

 <220>
 <221> PEPTIDE
 <222> (1)..(21)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residues 3,4 adn 5 may be Glu or Gla; Xaa at residues 10 and 18 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 14, 15, 16 and 17 may be Pro or hydroxy-Pro

 <400> 69
 Xaa Ser Xaa Xaa Xaa Lys Ile Cys Leu Xaa Lys Ile Cys Xaa Xaa Xaa
 1 5 10 15

 Xaa Xaa Arg Arg Ser
 20

 <210> 70
 <211> 398
 <212> DNA
 <213> Conus purpurascens

 <220>
 <221> CDS
 <222> (1)..(213)

 <400> 70
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
 1 5 10 15

 gcc cct ctg tct gag ggt aga aaa ccg aac gat gta att cgg ggt ttg 96
 Ala Pro Leu Ser Glu Gly Arg Lys Pro Asn Asp Val Ile Arg Gly Leu
 20 25 30

 gtg cca gat gac tta gcc cta cag ctt atc ttg caa agt cag gtt tcc 144
 Val Pro Asp Asp Leu Ala Leu Gln Leu Ile Leu Gln Ser Gln Val Ser
 35 40 45

 cgt cgt gaa tct aat ggg gtg gaa ata tgc atg tgg aag gta tgt cca 192
 Arg Arg Glu Ser Asn Gly Val Glu Ile Cys Met Trp Lys Val Cys Pro
 50 55 60

 cca tcc cca tgg aga cga tca taaggaaaaa aaatgaatga cgtcagacaa 243
 Pro Ser Pro Trp Arg Arg Ser
 65 70

 ccaccacaac tgtaatacga catcggttaac acgacttcag caaacatttt aacatcactg 303
 tggttgtgaa gaaatcagtt gctttaaaag attggatttt tccttggtta agagttgtac 363
 tgatatcagc tctgccctat gaaataaagc tgatg 398

<210> 71
 <211> 71
 <212> PRT
 <213> *Conus purpurascens*

<400> 71
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
 1 5 10 15
 Ala Pro Leu Ser Glu Gly Arg Lys Pro Asn Asp Val Ile Arg Gly Leu
 20 25 30
 Val Pro Asp Asp Leu Ala Leu Gln Leu Ile Leu Gln Ser Gln Val Ser
 35 40 45
 Arg Arg Glu Ser Asn Gly Val Glu Ile Cys Met Trp Lys Val Cys Pro
 50 55 60
 Pro Ser Pro Trp Arg Arg Ser
 65 70

<210> 72
 <211> 21
 <212> PRT
 <213> *Conus purpurascens*

<220>
 <221> PEPTIDE
 <222> (1)..(21)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 may be Glu
 or Glu; Xaa at residues 10 and 18 may be Trp (D or L) or bromo-Trp
 (D or L); Xaa at residues 14, 15 and 17 may be Pro or hydroxy-Pro

<400> 72
 Xaa Ser Asn Gly Val Xaa Ile Cys Met Xaa Lys Val Cys Xaa Xaa Ser
 1 5 10 15
 Xaa Xaa Arg Arg Ser
 20

<210> 73
 <211> 409
 <212> DNA
 <213> *Conus stercusmuscarum*

<220>
 <221> CDS
 <222> (1)..(213)

<400> 73
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
 1 5 10 15
 gcc cct ctg tct gaa ggt ggt aaa ttg acc gac gta att cgg ggt ttg 96
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Thr Asp Val Ile Arg Gly Leu
 20 25 30
 gtg cca cac atc tta acc cca cag cat atc ttg caa agt atg act tcc 144
 Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Met Thr Ser
 35 40 45
 cgt ctt ggt att ggc agc agt gat caa aat gca caa ata tgc atc tgg 192

Arg Leu Gly Ile Gly Ser Ser Asp Gln Asn Ala Gln Ile Cys Ile Trp
50 55 60

aag gta tgt cca cca tcc cca tagagacgac cataaggaaa aagatgaatg 243
Lys Val Cys Pro Pro Ser Pro
65 70

acgtcagaca accgccacaa ctgtagtacg acatcgttga tacgacttca gcaaataattt 303
taacatcact gtggttgtga agaaatcagt tgctttaaaa gattggattt ttccttgattt 363
aagagttgta ctgatatcag ctctgccctg tgaaataaag ctgatg 409

<210> 74
<211> 71
<212> PRT
<213> Conus stercusmuscarum

<400> 74
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
1 5 10 15
Ala Pro Leu Ser Glu Gly Gly Lys Leu Thr Asp Val Ile Arg Gly Leu
20 25 30
Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Met Thr Ser
35 40 45
Arg Leu Gly Ile Gly Ser Ser Asp Gln Asn Ala Gln Ile Cys Ile Trp
50 55 60
Lys Val Cys Pro Pro Ser Pro
65 70

<210> 75
<211> 22
<212> PRT
<213> Conus stercusmuscarum

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 15 may be Trp or bromo-Trp; Xaa at residue 19, 20
and 22 may be Pro or hydroxy-Pro

<400> 75
Leu Gly Ile Gly Ser Ser Asp Gln Asn Ala Gln Ile Cys Ile Xaa Lys
1 5 10 15
Val Cys Xaa Xaa Ser Xaa
20

<210> 76
<211> 433
<212> DNA
<213> Conus baileyi

<220>
<221> CDS
<222> (1)..(216)

<400> 76
atg cag acg gcc tac tgg gtg atg gtg atg ata atg gtg tgg att aca 48
Met Gln Thr Ala Tyr Trp Val Met Val Met Ile Met Val Trp Ile Thr


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1             5             10             15
gtc cct ctg tct gaa ggt ggt aaa ttg aac gac ata att cgg ggt ttg      96
Val Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Ile Ile Arg Gly Leu
                20                25                30

ttg cca gac aac ttc ccc cca cag ctt acc ttg cat cgt ctg gtt tcc      144
Leu Pro Asp Asn Phe Pro Pro Gln Leu Thr Leu His Arg Leu Val Ser
                35                40                45

cgt cgt cat tct gac agc att att ctg agg ggc tta tgt atc tgg aag      192
Arg Arg His Ser Asp Ser Ile Ile Leu Arg Gly Leu Cys Ile Trp Lys
                50                55                60

gtg tgt gaa cct ccg cca caa aga tgatctggtc caaagccaaa aaacgaatga      246
Val Cys Glu Pro Pro Pro Gln Arg
65                70

tgtcagacaa ccgccacagc tttagtacga catggttaat acgacttcag caaatatttc      306

aacatcactg tggttgtgaa gaaatcagtt actttaaaag attggaatga tgtcagctgt      366

gcactatcaa ataaagttga tgtgacaaaa aaaaaaaaaa aaaaagtact ctgcgttggt      426

actcgag                                                    433

<210>  77
<211>  72
<212>  PRT
<213>  Conus baileyi

<400>  77
Met Gln Thr Ala Tyr Trp Val Met Val Met Ile Met Val Trp Ile Thr
1             5             10             15

Val Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Ile Ile Arg Gly Leu
                20                25                30

Leu Pro Asp Asn Phe Pro Pro Gln Leu Thr Leu His Arg Leu Val Ser
                35                40                45

Arg Arg His Ser Asp Ser Ile Ile Leu Arg Gly Leu Cys Ile Trp Lys
                50                55                60

Val Cys Glu Pro Pro Pro Gln Arg
65                70

<210>  78
<211>  22
<212>  PRT
<213>  Conus baileyi

<220>
<221>  PEPTIDE
<222>  (1)..(22)
<223>  Xaa at residue 13 may be Trp (D or L) or bromo-Trp (D or L); Xaa
        at residue 17 may be Glu or Gla; Xaa at residues 18, 19 and 20 ma
        y be Pro or hydroxy-Pro

<400>  78
His Ser Asp Ser Ile Ile Leu Arg Gly Leu Cys Ile Xaa Lys Val Cys
1             5             10             15

Xaa Xaa Xaa Xaa Gln Arg

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20

<210> 79
 <211> 413
 <212> DNA
 <213> Conus bocki

<220>
 <221> CDS
 <222> (1)..(270)

<400> 79
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
 1 5 10 15
 gcc cct ctg tct gaa agt gat aaa ctg aac gac gta att cgg ggt ttg 96
 Ala Pro Leu Ser Glu Ser Asp Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30
 gtg cca gac aac tta acc cca cag ctt atc ttg cga agt ctg att tcc 144
 Val Pro Asp Asn Leu Thr Pro Gln Leu Ile Leu Arg Ser Leu Ile Ser
 35 40 45
 cgt cgt cgt tct gac aag gat gat ccg gga gga caa gaa tgt tac tgg 192
 Arg Arg Arg Ser Asp Lys Asp Asp Pro Gly Gly Gln Glu Cys Tyr Trp
 50 55 60
 aac gta tgt gca cca aac cag gga gac cac atg atc tta aga aaa aag 240
 Asn Val Cys Ala Pro Asn Gln Gly Asp His Met Ile Leu Arg Lys Lys
 65 70 75 80
 atg aat gac gac aga caa ccg cca caa ctg taatacgaca tcgttaatac 290
 Met Asn Asp Asp Arg Gln Pro Pro Gln Leu
 85 90
 gacttcagca aatatitttaa catcactgtg gttgtgaaga aatcagttgc tttaaaagat 350
 tggatttttc cgtgtttaag agctgtactg atatctgctc tgccctgtga aataaagctg 410
 atg 413

<210> 80
 <211> 90
 <212> PRT
 <213> Conus bocki

<400> 80
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
 1 5 10 15
 Ala Pro Leu Ser Glu Ser Asp Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30
 Val Pro Asp Asn Leu Thr Pro Gln Leu Ile Leu Arg Ser Leu Ile Ser
 35 40 45
 Arg Arg Arg Ser Asp Lys Asp Asp Pro Gly Gly Gln Glu Cys Tyr Trp
 50 55 60
 Asn Val Cys Ala Pro Asn Gln Gly Asp His Met Ile Leu Arg Lys Lys
 65 70 75 80
 Met Asn Asp Asp Arg Gln Pro Pro Gln Leu
 85 90

<210> 81
 <211> 40
 <212> PRT
 <213> Conus bocki

<220>
 <221> PEPTIDE
 <222> (1)..(40)
 <223> Xaa at residues 7, 19, 37, 38 may be Pro or hydroxy-Pro; Xaa at residue 11 may be Glu or Glu; Xaa at residue 14 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residue 13 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 81
 Arg Ser Asp Lys Asp Asp Xaa Gly Gly Gln Xaa Cys Xaa Xaa Asn Val
 1 5 10 15
 Cys Ala Xaa Asn Gln Gly Asp His Met Ile Leu Arg Lys Lys Met Asn
 20 25 30
 Asp Asp Arg Gln Xaa Xaa Gln Leu
 35 40

<210> 82
 <211> 496
 <212> DNA
 <213> Conus chaldaeus

<220>
 <221> CDS
 <222> (21)..(260)

<400> 82
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg atg ggg atg 53
 Met Gln Thr Ala Tyr Trp Val Met Met Gly Met
 1 5 10
 atg atg gtg tgg att aca gcc cct ctg tct gga ggt ggt aaa ctg aac 101
 Met Met Val Trp Ile Thr Ala Pro Leu Ser Gly Gly Lys Leu Asn
 15 20 25
 gac gta att cgg ggt ttg gtg cca gac gac tta acc cta cag cgt atg 149
 Asp Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Leu Gln Arg Met
 30 35 40
 ttc gaa act ccg gtt tcc cat cgt ctt tct gag ggc aga aat tcg acg 197
 Phe Glu Thr Pro Val Ser His Arg Leu Ser Glu Gly Arg Asn Ser Thr
 45 50 55
 gta cac ata tgt acg tgg aag gta tgt cca cct ccc cca tgg aga cga 245
 Val His Ile Cys Thr Trp Lys Val Cys Pro Pro Pro Trp Arg Arg
 60 65 70 75
 cca cat gga caa aga tgaatgacgt cagacaacct ccacaactgt agtacgacat 300
 Pro His Gly Gln Arg
 80
 cgtaaacacg acgtcagcta atcttttaac atcactgtgg ctgtgaagaa ctcggttgct 360
 ttaaaagatt ggatttttcc ttgtttaaga gttgtgctga tatgaactct gcactacgaa 420
 ataaagctga tgtgacaaac aaaaaaaaga aaaaaaaaag tactctgcgt tggtactcga 480
 gcttaagggc gaattc 496

<210> 83
 <211> 80
 <212> PRT
 <213> Conus chaldaeus

<400> 83
 Met Gln Thr Ala Tyr Trp Val Met Met Gly Met Met Met Val Trp Ile
 1 5 10 15
 Thr Ala Pro Leu Ser Gly Gly Gly Lys Leu Asn Asp Val Ile Arg Gly
 20 25 30
 Leu Val Pro Asp Asp Leu Thr Leu Gln Arg Met Phe Glu Thr Pro Val
 35 40 45
 Ser His Arg Leu Ser Glu Gly Arg Asn Ser Thr Val His Ile Cys Thr
 50 55 60
 Trp Lys Val Cys Pro Pro Pro Pro Trp Arg Arg Pro His Gly Gln Arg
 65 70 75 80

<210> 84
 <211> 29
 <212> PRT
 <213> Conus chaldaeus

<220>
 <221> PEPTIDE
 <222> (1)..(29)
 <223> Xaa at residue 3 may be Glu or Gla; Xaa at residues 14 and 22 may
 be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 18, 19, 2
 0, 21 and 25 may be Pro or hydroxy-Pro

<400> 84
 Leu Ser Xaa Gly Arg Asn Ser Thr Val His Ile Cys Thr Xaa Lys Val
 1 5 10 15
 Cys Xaa Xaa Xaa Xaa Xaa Arg Arg Xaa His Gly Gln Arg
 20 25

<210> 85
 <211> 499
 <212> DNA
 <213> Conus chaldaeus

<220>
 <221> CDS
 <222> (21)..(260)

<400> 85
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg atg ggg atg 53
 Met Gln Thr Ala Tyr Trp Val Met Met Gly Met
 1 5 10
 atg atg gtg tgg att aca gcc cct ctg tct gga ggt ggt aaa ctg aac 101
 Met Met Val Trp Ile Thr Ala Pro Leu Ser Gly Gly Gly Lys Leu Asn
 15 20 25
 gac gta att cgg ggt ttg gtg cca gac gac tta acc cta cag cgt atg 149
 Asp Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Leu Gln Arg Met
 30 35 40
 ttc gaa act ccg gtt tcc cat cgt ctt tct gag ggc aga aat tcg acg 197

Phe Glu Thr Pro Val Ser His Arg Leu Ser Glu Gly Arg Asn Ser Thr
 45 50 55
 gta cac ata tgt atg tgg aag gta tgt cca cct ccc cca tgg aga cga 245
 Val His Ile Cys Met Trp Lys Val Cys Pro Pro Pro Pro Trp Arg Arg
 60 65 70 75
 cca cat gga caa aga tgaatgacgt cagacaacct ccacaactgt agtacgacat 300
 Pro His Gly Gln Arg
 80
 cgттаacacg acgtcagcta atcttttaac atcactgtgg ttgtgaagaa atcggttgct 360
 ttaaaagatt ggatttttcc ttgtttaaga gttgtgctga tatgaactct gcactacgaa 420
 ataaagctga tgtgacaaac ggaaaaaaaa aaaaaaaaaa aagtactctg cgttgttact 480
 cgagcttaag ggcgaattc 499
 <210> 86
 <211> 80
 <212> PRT
 <213> Conus chaldaeus
 <400> 86
 Met Gln Thr Ala Tyr Trp Val Met Met Gly Met Met Met Val Trp Ile
 1 5 10 15
 Thr Ala Pro Leu Ser Gly Gly Gly Lys Leu Asn Asp Val Ile Arg Gly
 20 25 30
 Leu Val Pro Asp Asp Leu Thr Leu Gln Arg Met Phe Glu Thr Pro Val
 35 40 45
 Ser His Arg Leu Ser Glu Gly Arg Asn Ser Thr Val His Ile Cys Met
 50 55 60
 Trp Lys Val Cys Pro Pro Pro Pro Trp Arg Arg Pro His Gly Gln Arg
 65 70 75 80
 <210> 87
 <211> 29
 <212> PRT
 <213> Conus chaldaeus
 <220>
 <221> PEPTIDE
 <222> (1)..(29)
 <223> Xaa at residue 3 may be Glu or Gla; Xaa at residues 14 and 22 may
 be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 18, 19, 2
 0, 21 and 25 may be Pro or hydroxy-Pro
 <400> 87
 Leu Ser Xaa Gly Arg Asn Ser Thr Val His Ile Cys Met Xaa Lys Val
 1 5 10 15
 Cys Xaa Xaa Xaa Xaa Xaa Arg Arg Xaa His Gly Gln Arg
 20 25
 <210> 88
 <211> 490
 <212> DNA
 <213> Conus cinereus
 <220>

<221> CDS

<222> (21)..(305)

<400> 88

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gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg      53
          Met Gln Thr Ala Tyr Trp Val Met Val Met Met
              1              5              10

```

```

ttg gtg tgg att aca gcc cct ctg cct gag ggt ggt aaa ccg aag cac      101
Leu Val Trp Ile Thr Ala Pro Leu Pro Glu Gly Gly Lys Pro Lys His
              15              20              25

```

```

gta att cgg ggt ttg gta cca gac gac tta acc cca cag cat atc ttg      149
Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Pro Gln His Ile Leu
              30              35              40

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```

cga agt ttg att tcc cgt cgt tca tct ggc tgc agt gtt tcg ttg ggc      197
Arg Ser Leu Ile Ser Arg Arg Ser Ser Gly Cys Ser Val Ser Leu Gly
              45              50              55

```

```

ttc aaa tgc ttc tgg aag agc tgt aca gta atc cca gtg aga cca ttt      245
Phe Lys Cys Phe Trp Lys Ser Cys Thr Val Ile Pro Val Arg Pro Phe
              60              65              70              75

```

```

gta tct ctg gaa gaa gaa aat gaa tgc cag aaa gtc caa ata agt gca      293
Val Ser Leu Glu Glu Glu Asn Glu Cys Gln Lys Val Gln Ile Ser Ala
              80              85              90

```

```

gta tgg ggt cct tgatacgact tcagcaagga tcactgtggt tgtgaagaaa      345
Val Trp Gly Pro
              95

```

```

tcagttgctt taaaagattt gatttttctt tgtttaagag ttgtactgat atcagctctg      405

```

```

tactatgaaa taaagctgat gtgacaaaaca aaaaaaaaaa aaaaaaaagt actctgcggt      465

```

```

gttactcgag cttaagggcg aattc      490

```

<210> 89

<211> 95

<212> PRT

<213> Conus cinereus

<400> 89

```

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Leu Val Trp Ile Thr
1              5              10              15

```

```

Ala Pro Leu Pro Glu Gly Gly Lys Pro Lys His Val Ile Arg Gly Leu
20              25              30

```

```

Val Pro Asp Asp Leu Thr Pro Gln His Ile Leu Arg Ser Leu Ile Ser
35              40              45

```

```

Arg Arg Ser Ser Gly Cys Ser Val Ser Leu Gly Phe Lys Cys Phe Trp
50              55              60

```

```

Lys Ser Cys Thr Val Ile Pro Val Arg Pro Phe Val Ser Leu Glu Glu
65              70              75              80

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Glu Asn Glu Cys Gln Lys Val Gln Ile Ser Ala Val Trp Gly Pro
85              90              95

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<210> 90

<211> 45

<212> PRT

<213> Conus cinereus

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<221> PEPTIDE

<222> (1)..(45)

<223> Xaa at residues 14 and 43 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 21, 24 and 45 may be Pro or hydroxy-Pro; Xaa at residues 29, 30, 31 and 33 may be Glu or Gla

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Ser Ser Gly Cys Ser Val Ser Leu Gly Phe Lys Cys Phe Xaa Lys Ser
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Cys Thr Val Ile Xaa Val Arg Xaa Phe Val Ser Leu Xaa Xaa Xaa Asn
20 25 30

Xaa Cys Gln Lys Val Gln Ile Ser Ala Val Xaa Gly Xaa
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<211> 497

<212> DNA

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<222> (21)..(263)

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Met Gln Thr Ala Tyr Trp Val Met Val Met Met
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gtg gtg gtg tgg att aca gcc cct ctg cct gaa ggt ggt aaa ccg gag 101
Val Val Val Trp Ile Thr Ala Pro Leu Pro Glu Gly Gly Lys Pro Glu
15 20 25

cac gta att cgg ggt ttg gtg cca gac gac tta acc cca cag ctt atc 149
His Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Pro Gln Leu Ile
30 35 40

ttg cga agt ctg att tcc cgt cgt agt tct gac ggc aag gca aaa aga 197
Leu Arg Ser Leu Ile Ser Arg Arg Ser Ser Asp Gly Lys Ala Lys Arg
45 50 55

aat tgt ttc tgg aag gca tgt gta cca gaa caa tgg aga caa cgt gat 245
Asn Cys Phe Trp Lys Ala Cys Val Pro Glu Gln Trp Arg Gln Arg Asp
60 65 70 75

ctt aag gaa aaa gat gaa tgatgtcaga caaccgccat cactgtagta 293
Leu Lys Glu Lys Asp Glu
80

tgacatcggtt aatacgactt aagcaaatat ttaaacatca ctgtggatct gaagaaatca 353

gttgcttttaa aagattggat ttttcctcgt ttaagagttg tactgatgtc agctctgcac 413

tgtgaaataa agctgatgtg acaaacgaaa aaaaaaaaaa aaaaaaagta ctctgcggtg 473

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<210> 92

<211> 81

<212> PRT

<213> Conus cinereus

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 35 40 45
 Ser Arg Arg Ser Ser Asp Gly Lys Ala Lys Arg Asn Cys Phe Trp Lys
 50 55 60
 Ala Cys Val Pro Glu Gln Trp Arg Gln Arg Asp Leu Lys Glu Lys Asp
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 Glu

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 Xaa Xaa Gln Xaa Arg Gln Arg Asp Leu Lys Xaa Lys Asp Xaa
 20 25 30

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<400> 94
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 1 5 10
 atg gtg gtg tgg att aca gcc cct ctg cct gaa ggt ggt aaa ccg aag 101
 Met Val Val Trp Ile Thr Ala Pro Leu Pro Glu Gly Gly Lys Pro Lys
 15 20 25
 cac gta att cgg ggt ttg gtg cca gac gac tta acc cca cag ctt atc 149
 His Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Pro Gln Leu Ile
 30 35 40
 ttg cga agt ctg att tcc cgt cgt agt tct gac ggc aag gca aaa aga 197
 Leu Arg Ser Leu Ile Ser Arg Arg Ser Ser Asp Gly Lys Ala Lys Arg
 45 50 55

aat tgt ttc tgg aag gca tgt gta cca gaa caa tgg aga caa cgt gat 245
 Asn Cys Phe Trp Lys Ala Cys Val Pro Glu Gln Trp Arg Gln Arg Asp
 60 65 70 75

cct aag gaa aaa gat gaa tgatgtcaga caaccgccat cactgtagta 293
 Pro Lys Glu Lys Asp Glu
 80

tgacatcggt aatacgactt aagcaaatat ttttaacatca ctgtggatct gaagaaatca 353

gttgcttttaa aagattggat ttttcctcgt ttaagagttg tactgatgtc agctctgcac 413

tgtgaaataa agctgacgtg acaagcaaaa aaaaaaaaaa aaaaaagtac tctgcgttgt 473

tactcgagct taagggcgaa ttc 496

<210> 95

<211> 81

<212> PRT

<213> Conus cinereus

<400> 95

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Trp Ile
 1 5 10 15

Thr Ala Pro Leu Pro Glu Gly Gly Lys Pro Lys His Val Ile Arg Gly
 20 25 30

Leu Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Arg Ser Leu Ile
 35 40 45

Ser Arg Arg Ser Ser Asp Gly Lys Ala Lys Arg Asn Cys Phe Trp Lys
 50 55 60

Ala Cys Val Pro Glu Gln Trp Arg Gln Arg Asp Pro Lys Glu Lys Asp
 65 70 75 80

Glu

<210> 96

<211> 30

<212> PRT

<213> Conus cinereus

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<222> (1)..(30)

<223> Xaa at residues 12 and 20 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 17 and 25 may be Pro or hydroxy-Pro; Xaa at residues 18, 27 and 30 may be Glu or Gla

<400> 96

Ser Ser Asp Gly Lys Ala Lys Arg Asn Cys Phe Xaa Lys Ala Cys Val
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Xaa Xaa Gln Xaa Arg Gln Arg Asp Xaa Lys Xaa Lys Asp Xaa
 20 25 30

<210> 97

<211> 493

<212> DNA

<213> Conus cinereus

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<222> (21)..(260)

<400> 97

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          1              5              10

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atg gtg tgg att aca gcc cct ctg tct gaa ggt ggt aaa ccg aag cac      101
Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Pro Lys His
          15              20              25

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gta att cgg ggt ttg gtg cca gtc gac tta acc cca cag ctt atc ttg      149
Val Ile Arg Gly Leu Val Pro Val Asp Leu Thr Pro Gln Leu Ile Leu
          30              35              40

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cga agt ctg att tcc cgt cgt agt tct gac ggc aag gca aaa aaa caa      197
Arg Ser Leu Ile Ser Arg Arg Ser Ser Asp Gly Lys Ala Lys Lys Gln
          45              50              55

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tgt gcc tgg aag aca tgt gta cca acc caa tgg aga cga cgt gat ctt      245
Cys Ala Trp Lys Thr Cys Val Pro Thr Gln Trp Arg Arg Arg Asp Leu
          60              65              70              75

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aag gaa aaa gat gaa tgatgtcaga caaccgccat cactgtagta tgacatcgtt      300
Lys Glu Lys Asp Glu
          80

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aatacgactt aagcaaatat ttttaacatca ctgtggttct gaagaaatca gttgctttaa      360

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aagattggat ttttccttgt ttaagagttg tactgatatc agctctgcac tgtgaaataa      420

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agctgatgtg acaaacaaaa aaaaaaaaaa aaaaaagtac tctgcgttgt tactcgagct      480

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taagggcgaa ttc      493

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<210> 98

<211> 80

<212> PRT

<213> Conus cinereus

<400> 98

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Met Gln Thr Ala Tyr Trp Val Met Val Ile Met Met Val Trp Ile Thr
1              5              10              15

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Ala Pro Leu Ser Glu Gly Gly Lys Pro Lys His Val Ile Arg Gly Leu
          20              25              30

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Val Pro Val Asp Leu Thr Pro Gln Leu Ile Leu Arg Ser Leu Ile Ser
          35              40              45

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Arg Arg Ser Ser Asp Gly Lys Ala Lys Lys Gln Cys Ala Trp Lys Thr
          50              55              60

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Cys Val Pro Thr Gln Trp Arg Arg Arg Asp Leu Lys Glu Lys Asp Glu
          65              70              75              80

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<210> 99

<211> 30

<212> PRT

<213> Conus cinereus

<220>

<221> PEPTIDE

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<222> (1)..(30)
 <223> Xaa at residues 12 and 20 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residue 17 may be Pro or hydroxy-Pro; Xaa at residues 27 and 30 may be Glu or Gla

 <400> 99
 Ser Ser Asp Gly Lys Ala Lys Lys Gln Cys Ala Xaa Lys Thr Cys Val
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 Xaa Thr Gln Xaa Arg Arg Arg Asp Leu Lys Xaa Lys Asp Xaa
 20 25 30

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 atg gtg tgg att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac 101
 Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp
 15 20 25

 gta att cgg ggt ttg gtg cca cac atc tta acc cca cag cat atc ttg 149
 Val Ile Arg Gly Leu Val Pro His Ile Leu Thr Pro Gln His Ile Leu
 30 35 40

 caa ggt ctg act tcc cgt ctt cgt tct gac agc agt ggt cag aaa gga 197
 Gln Gly Leu Thr Ser Arg Leu Arg Ser Asp Ser Ser Gly Gln Lys Gly
 45 50 55

 gca caa ata tgc atc tgg aag gta tgt cca cta tcc cca tgg aga cga 245
 Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Leu Ser Pro Trp Arg Arg
 60 65 70 75

 cca caa gga aaa gat gaa tgacgtcaga caaccgctac aactgtagta 293
 Pro Gln Gly Lys Asp Glu
 80

 cgacatcggt gatacgactt cagcaaatat ttttaacatca ctgtggttgt gaagaaatca 353

 gctgctttaa aagattggat ttttccttgt ttaagagttg tactgatatc agctctgcac 413

 tatgaaataa agctgatgtg acaaacacaaa aaaaaaaaaa aaaaaagtac tctgcgttgt 473

 tactcgagct taagggcgaa ttc 496

 <210> 101
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 <400> 101
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
 1 5 10 15

 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu

	20		25		30										
Val	Pro	His	Ile	Leu	Thr	Pro	Gln	His	Ile	Leu	Gln	Gly	Leu	Thr	Ser
	35					40					45				
Arg	Leu	Arg	Ser	Asp	Ser	Ser	Gly	Gln	Lys	Gly	Ala	Gln	Ile	Cys	Ile
	50				55					60					
Trp	Lys	Val	Cys	Pro	Leu	Ser	Pro	Trp	Arg	Arg	Pro	Gln	Gly	Lys	Asp
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Glu

<210> 102
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<400>	102														
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1		5						10					15		
Lys	Val	Cys	Xaa	Leu	Ser	Xaa	Xaa	Arg	Arg	Xaa	Gln	Gly	Lys	Asp	Xaa
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Met Val Trp	Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp		
	15 20 25		
gta att cgg ggt ttg gtg cca cac ttc tta acc cca cag cat atc ttg		149	
Val Ile Arg Gly Leu Val Pro His Phe Leu Thr Pro Gln His Ile Leu			
	30 35 40		
caa agt ctg act tcc cgt aat ggt tct ggc agc agt aat cag aaa gaa		197	
Gln Ser Leu Thr Ser Arg Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu			
	45 50 55		
gca caa cta tgc atc tgg aag gta tgt cca cca acc cca tgg aga		242	
Ala Gln Leu Cys Ile Trp Lys Val Cys Pro Thr Pro Trp Arg			
	60 65 70		
tgaccacaag	gaaaaagatg aacggcgtca gacaaccgcc acaactgtag tgggacatcg	302	

ttgatacgac ttcagcaaatt attttaacat cactgtgggt gtgaagaaat cagttgtttt 362
 aaaagattgg atttttcctt gtttaagagt tgtactgata tcagctctgc actatgaaat 422
 aaagctgatg tgacaagcaa aaaaaaaaaa aaaaaaagta ctctgcgttg ttactcgagc 482
 ttaagggcga attc 496

<210> 104
 <211> 74
 <212> PRT
 <213> Conus consors

<400> 104
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Val Trp Ile Thr
 1 5 10 15
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30
 Val Pro His Phe Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser
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 Arg Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu Ala Gln Leu Cys Ile
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 Trp Lys Val Cys Pro Pro Thr Pro Trp Arg
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<210> 105
 <211> 25
 <212> PRT
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<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 10 may be Glu or Gla ; Xaa at residues 16 and 24 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 20, 21 and 23 may be Pro or hydroxy-Pro

<400> 105
 Asn Gly Ser Gly Ser Ser Asn Gln Lys Xaa Ala Gln Leu Cys Ile Xaa
 1 5 10 15
 Lys Val Cys Xaa Xaa Thr Xaa Xaa Arg
 20 25

<210> 106
 <211> 496
 <212> DNA
 <213> Conus consors

<220>
 <221> CDS
 <222> (21)..(242)

<400> 106
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met
 1 5 10
 atg gtg tgg att aca gcc cct ctg tct gaa ggt ggt aaa ctg aac ggc 101
 Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Gly

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                15                20                25
gta att cgg ggt ttg gtg tca cac atc tta atc cca cag cat acc ttg      149
Val Ile Arg Gly Leu Val Ser His Ile Leu Ile Pro Gln His Thr Leu
                30                35                40

cga agt ctg act tcc cgt gat cgt tct gac aac ggt ggt tcg agt gga      197
Arg Ser Leu Thr Ser Arg Asp Arg Ser Asp Asn Gly Gly Ser Ser Gly
                45                50                55

gca caa ata tgc atc tgg aag gta tgt cca cca tcc cca tgg aaa      242
Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Ser Pro Trp Lys
        60                65                70

tgaccacaag gaaaaagatg aacggcgtca gacaaccacc acaactgtag tgggacatcg      302

ttgatacgac tttagcaaat attttaacat cactgtggtc gtgaagaaat cagttgcttt      362

aaaagattgg atttttcctt gtttaagagt tgtactgata tcagctctgc actatgaaat      422

aaagctgatg tgacaaacaa aaaaaaaaaa aaaaaaagta ctctgcgttg ttactcgagc      482

ttaagggcga attc      496

<210> 107
<211> 74
<212> PRT
<213> Conus consors

<400> 107
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
1                5                10                15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Gly Val Ile Arg Gly Leu
                20                25                30

Val Ser His Ile Leu Ile Pro Gln His Thr Leu Arg Ser Leu Thr Ser
                35                40                45

Arg Asp Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile
        50                55                60

Trp Lys Val Cys Pro Pro Ser Pro Trp Lys
        65                70

<210> 108
<211> 25
<212> PRT
<213> Conus consors

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residues 16 and 24 may be Trp (D or L) or bromo-Trp (D or
        L); Xaa at residues 20, 21 and 23 may be Pro or hydroxy-Pro

<400> 108
Asp Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Xaa
1                5                10                15

Lys Val Cys Xaa Xaa Ser Xaa Xaa Lys
        20                25

<210> 109

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<211> 459
 <212> DNA
 <213> Conus coronatus

<220>
 <221> CDS
 <222> (1)..(240)

<400> 109
 atg cag acg gcc tac tgg gtg atg atg atg atg atg atg atg tgg att 48
 Met Gln Thr Ala Tyr Trp Val Met Met Met Met Met Met Val Trp Ile
 1 5 10 15
 aca gcc cct ctg tct gaa ggt ggt aaa ctg aac gac gta att cgg ggt 96
 Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly
 20 25 30
 ttg gtg cca gac gac tta acc cta cag cgt atg ttc aaa gct ctg gtt 144
 Leu Val Pro Asp Asp Leu Thr Leu Gln Arg Met Phe Lys Ala Leu Val
 35 40 45
 tcc cat cgt ctt tct gac ggc aga gat tgg acg gga tac ata tgt atc 192
 Ser His Arg Leu Ser Asp Gly Arg Asp Trp Thr Gly Tyr Ile Cys Ile
 50 55 60
 tgg aag gca tgt cca cgt ccc cca tgg atc cca cca aag gga aaa aga 240
 Trp Lys Ala Cys Pro Arg Pro Pro Trp Ile Pro Pro Lys Gly Lys Arg
 65 70 75 80
 tgaatgacgt cagacaaccg ccacaactgt agtacgacat cgtaaacaca acttcagcta 300
 atattttaac atcactgtgg ttgtgaagaa atcggttgct ttaaaagatt gaatttttcg 360
 tttaagagtt gtgctgatac gagctctgca ctatgaaata aagctgatgt gacaaacaaa 420
 aaaaaaaaaa aaaaaaagta ctctgcgttg ttactcgag 459

<210> 110
 <211> 80
 <212> PRT
 <213> Conus coronatus

<400> 110
 Met Gln Thr Ala Tyr Trp Val Met Met Met Met Met Met Val Trp Ile
 1 5 10 15
 Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly
 20 25 30
 Leu Val Pro Asp Asp Leu Thr Leu Gln Arg Met Phe Lys Ala Leu Val
 35 40 45
 Ser His Arg Leu Ser Asp Gly Arg Asp Trp Thr Gly Tyr Ile Cys Ile
 50 55 60
 Trp Lys Ala Cys Pro Arg Pro Pro Trp Ile Pro Pro Lys Gly Lys Arg
 65 70 75 80

<210> 111
 <211> 26
 <212> PRT
 <213> Conus coronatus

<220>
 <221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residues 7, 14 and 22 may be Trp or bromo-Trp; Xaa at residue 10 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 18, 29, 21, 24 and 25 may be Pro or hydroxy-Pro

<400> 111

Leu Ser Asp Gly Arg Asp Xaa Thr Gly Xaa Ile Cys Ile Xaa Lys Ala
1 5 10 15

Cys Xaa Arg Xaa Xaa Xaa Ile Xaa Xaa Lys
20 25

<210> 112

<211> 495

<212> DNA

<213> Conus ebraeus

<220>

<221> CDS

<222> (21)..(236)

<400> 112

gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg atg atg atg 53
Met Gln Thr Ala Tyr Trp Val Met Met Met Met
1 5 10

atg atg gtg tgg att aca gcc cct ctg tct gaa ggc ggt aaa ctg aac 101
Met Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn
15 20 25

gac gta att cgg ggt ttg gtg cca gac gac tta acc cta cag cgt atg 149
Asp Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Leu Gln Arg Met
30 35 40

ttc aaa agt ctg ttt tcc cat cgt ctt tct ggc ggc aca tat tcg agg 197
Phe Lys Ser Leu Phe Ser His Arg Leu Ser Gly Gly Thr Tyr Ser Arg
45 50 55

gta gac aca tgc atc tgg aag gta tgt cca caa tct cca tagggacgat 246
Val Asp Thr Cys Ile Trp Lys Val Cys Pro Gln Ser Pro
60 65 70

catatggaaa aagatgagt acatcagaca actgccacaa ctgtagtacg acatcggttaa 306

cacgacttca gctaataatt taacatcact gtgggtgtga agaaatcggg tgctttaaaa 366

gattggattt ttccttgttt aagagttgtg ctgatatgag ctctgcacta tgaaataaag 426

ctgatgtgac aaacaaaaaa aaaaaaaaaa aagtactctg cgttgttact cgagcttaag 486

ggcgaattc 495

<210> 113

<211> 72

<212> PRT

<213> Conus ebraeus

<400> 113

Met Gln Thr Ala Tyr Trp Val Met Met Met Met Met Val Trp Ile
1 5 10 15

Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly
20 25 30

20250606 14:00:00

Leu Val Pro Asp Asp Leu Thr Leu Gln Arg Met Phe Lys Ser Leu Phe
35 40 45

Ser His Arg Leu Ser Gly Gly Thr Tyr Ser Arg Val Asp Thr Cys Ile
50 55 60

Trp Lys Val Cys Pro Gln Ser Pro
65 70

<210> 114

<211> 21

<212> PRT

<213> Conus ebraeus

<220>

<221> PEPTIDE

<222> (1)..(21)

<223> Xaa at residue 6 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 18 and 21 may be Pro or hydroxy-Pro

<400> 114

Leu Ser Gly Gly Thr Xaa Ser Arg Val Asp Thr Cys Ile Xaa Lys Val
1 5 10 15

Cys Xaa Gln Ser Xaa
20

<210> 115

<211> 537

<212> DNA

<213> Conus geographus

<220>

<221> CDS

<222> (21)..(299)

<400> 115

gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg ctg atg atg 53
Met Gln Thr Ala Tyr Trp Val Met Leu Met Met
1 5 10

atg gtg tgc atc aca gcc cct ctg cct gaa ggt ggt aaa ccg aac agc 101
Met Val Cys Ile Thr Ala Pro Leu Pro Glu Gly Gly Lys Pro Asn Ser
15 20 25

gga att cgg ggt ttg gtg cca aac gac tta act cca cag cat acc ttg 149
Gly Ile Arg Gly Leu Val Pro Asn Asp Leu Thr Pro Gln His Thr Leu
30 35 40

cga agt ctg att tcc cgt cgt caa act gac gtt ctt ctg gag gct acc 197
Arg Ser Leu Ile Ser Arg Arg Gln Thr Asp Val Leu Leu Glu Ala Thr
45 50 55

ctt ttg aca aca cca gcc ccc gag cag aga ttg ttc tgc ttc tgg aag 245
Leu Leu Thr Thr Pro Ala Pro Glu Gln Arg Leu Phe Cys Phe Trp Lys
60 65 70 75

tca tgt acg tgg agg ccc tac cct tgg aga cga cgt gat ctt aat gga 293
Ser Cys Thr Trp Arg Pro Tyr Pro Trp Arg Arg Asp Leu Asn Gly
80 85 90

aaa cga tgaatgacgc cagacaaccg ccacaactgt agtacgacat cgtaataacg 349

Lys Arg

acttcagcaa acattttaac ataactgtgg ttgtgaagaa atcagttgct ttaaaagatt 409
 ggattttttcc ttgtttcaga gttgtactga tatgagctct gcaccatgaa ataaagctga 469
 agtgacgaac aaaaaaaaaa aaaaaaaaaa agtactctgc gttgttactc gagcttaagg 529
 gcgaattc 537

<210> 116
 <211> 93
 <212> PRT
 <213> Conus geographus

<400> 116
 Met Gln Thr Ala Tyr Trp Val Met Leu Met Met Met Val Cys Ile Thr
 1 5 10 15
 Ala Pro Leu Pro Glu Gly Gly Lys Pro Asn Ser Gly Ile Arg Gly Leu
 20 25 30
 Val Pro Asn Asp Leu Thr Pro Gln His Thr Leu Arg Ser Leu Ile Ser
 35 40 45
 Arg Arg Gln Thr Asp Val Leu Leu Glu Ala Thr Leu Leu Thr Thr Pro
 50 55 60
 Ala Pro Glu Gln Arg Leu Phe Cys Phe Trp Lys Ser Cys Thr Trp Arg
 65 70 75 80
 Pro Tyr Pro Trp Arg Arg Arg Asp Leu Asn Gly Lys Arg
 85 90

<210> 117
 <211> 40
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(40)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residues 7 and 17 may be Glu or Gla; Xaa at residues 14, 16, 31 and 33 may be Pro or hydroxy-Pro; Xaa at residues 24, 29 and 34 may be Trp (D or L) or bromo-Trp (D or L)

<220>
 <221> PEPTIDE
 <222> (1)..(40)
 <223> Xaa at residue 32 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 117
 Xaa Thr Asp Val Leu Leu Xaa Ala Thr Leu Leu Thr Thr Xaa Ala Xaa
 1 5 10 15
 Xaa Gln Arg Leu Phe Cys Phe Xaa Lys Ser Cys Thr Xaa Arg Xaa Xaa
 20 25 30
 Xaa Xaa Arg Arg Arg Asp Leu Asn
 35 40

206330E3330

<210> 120

<211> 32
 <212> PRT
 <213> Conus gladiator

<220>
 <221> PEPTIDE
 <222> (1)..(32)
 <223> Xaa at residues 3, 18, 19, 21, 25, 27 and 29 may be Pro or hydrox
 y-Pro; Xaa at residues 14 and 20 may be Trp (D or L) or bromo-Trp
 (D or L)

<400> 120
 His Xaa Ala Asn Val Arg Gln Gln Gly Lys Ile Cys Val Xaa Lys Val
 1 5 10 15
 Cys Xaa Xaa Xaa Xaa Val Arg Ser Xaa Gly Xaa Gln Xaa Lys Asn Lys
 20 25 30

<210> 121
 <211> 459
 <212> DNA
 <213> Conus gladiator

<220>
 <221> CDS
 <222> (1)..(246)

<400> 121
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg gtt aca 48
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Val Thr
 1 5 10 15
 gtc cct cga tct gaa ggt ggc acg tgg aac tac tta att cgg ggt ttg 96
 Val Pro Arg Ser Glu Gly Gly Thr Trp Asn Tyr Leu Ile Arg Gly Leu
 20 25 30
 gtg cca gac gac cta acc cca cag ctt acc ttg cat cgt ctg gtt acc 144
 Val Pro Asp Asp Leu Thr Pro Gln Leu Thr Leu His Arg Leu Val Thr
 35 40 45
 cgt cgt cat cct gcc aac gtt aga cag cag ggg aaa ata tgt gta tgg 192
 Arg Arg His Pro Ala Asn Val Arg Gln Gln Gly Lys Ile Cys Val Trp
 50 55 60
 aag gtg tgt cca cca tcg cca gta aga tca cct ggt cca ctg cca aaa 240
 Lys Val Cys Pro Pro Ser Pro Val Arg Ser Pro Gly Pro Leu Pro Lys
 65 70 75 80
 aac aaa tgacgtcaga caaccgccac aacttttagta cgacatcggt gatacaactt 296
 Asn Lys
 cagcaagtat ttttaacatca ctgtggctct gaagaaatca gttgctttta aagattggat 356
 ttttccttgt ttttagagttt tactgatatc agctctgcac tatgaaataa agatgtgacg 416
 gacaaaaaaaa aaaaaaaaaa agtactctgc gttgttactc gag 459

<210> 122
 <211> 82
 <212> PRT
 <213> Conus gladiator

<400> 122

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Val Thr
 1 5 10 15
 Val Pro Arg Ser Glu Gly Gly Thr Trp Asn Tyr Leu Ile Arg Gly Leu
 20 25 30
 Val Pro Asp Asp Leu Thr Pro Gln Leu Thr Leu His Arg Leu Val Thr
 35 40 45
 Arg Arg His Pro Ala Asn Val Arg Gln Gln Gly Lys Ile Cys Val Trp
 50 55 60
 Lys Val Cys Pro Pro Ser Pro Val Arg Ser Pro Gly Pro Leu Pro Lys
 65 70 75 80

Asn Lys

<210> 123
 <211> 32
 <212> PRT
 <213> Conus gladiator
 <220>
 <221> PEPTIDE
 <222> (1)..(32)
 <223> Xaa at residues 2, 18, 19, 21, 25, 27 and 29 may be Pro or hydrox
 y-Pro; Xaa at residue 14 may be Trp (D or L) or bromo-Trp (D or L
)

<400> 123
 His Xaa Ala Asn Val Arg Gln Gln Gly Lys Ile Cys Val Xaa Lys Val
 1 5 10 15
 Cys Xaa Xaa Ser Xaa Val Arg Ser Xaa Gly Xaa Leu Xaa Lys Asn Lys
 20 25 30

<210> 124
 <211> 499
 <212> DNA
 <213> Conus litoglyphus

<220>
 <221> CDS
 <222> (21)..(254)

<400> 124
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met
 1 5 10
 atg gtg tgg att aca gcc cct ctg tct gaa ggt gat aaa ttg aac gac 101
 Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Asp Lys Leu Asn Asp
 15 20 25
 gta att cgg ggt ttg gtg cca gat aac tta gcc cca cag ctt gtt ttg 149
 Val Ile Arg Gly Leu Val Pro Asp Asn Leu Ala Pro Gln Leu Val Leu
 30 35 40
 caa agt ctg gat tcc cgt cgt cat cct cac ggc att cgt cag gat gga 197
 Gln Ser Leu Asp Ser Arg Arg His Pro His Gly Ile Arg Gln Asp Gly
 45 50 55
 gcc caa ata tgt atc tgg aag ata tgt cca cca tcc cca tgg aga cga 245
 Ala Gln Ile Cys Ile Trp Lys Ile Cys Pro Pro Ser Pro Trp Arg Arg

60	65	70	75	
ctt gga tct taagaaaaga aacaattgac gtcagacaac cgccacatct				294
Leu Gly Ser				
tgagtacgac atcgttaata cgacttcagc aaatatgaaa ttttcagcat cactgtggtt				354
gtgaagaaat cagttgcttt aaaagattgg atttgtcctt gtttaagagt tgtactgatg				414
tcatctctgc actatgaaat aaagctgatg tgaaaaaaaa aaaaaaaagt actctgcggt				474
gttactcgag cttaagggcg aattc				499
<210>	125			
<211>	78			
<212>	PRT			
<213>	Conus litoglyphus			
<400>	125			
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr				
1	5	10	15	
Ala Pro Leu Ser Glu Gly Asp Lys Leu Asn Asp Val Ile Arg Gly Leu				
	20	25	30	
Val Pro Asp Asn Leu Ala Pro Gln Leu Val Leu Gln Ser Leu Asp Ser				
	35	40	45	
Arg Arg His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile				
	50	55	60	
Trp Lys Ile Cys Pro Pro Ser Pro Trp Arg Arg Leu Gly Ser				
	65	70	75	
<210>	126			
<211>	28			
<212>	PRT			
<213>	Conus litoglyphus			
<220>				
<221>	PEPTIDE			
<222>	(1)..(28)			
<223>	Xaa at residues 2, 19, 20 and 22 may be Pro or hydroxy-Pro; Xaa at residues 15 and 23 may be Trp (D or L) or bromo-Trp (D or L)			
<400>	126			
His Xaa His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile Xaa Lys				
1	5	10	15	
Ile Cys Xaa Xaa Ser Xaa Xaa Arg Arg Leu Gly Ser				
	20	25		
<210>	127			
<211>	507			
<212>	DNA			
<213>	Conus litoglyphus			
<220>				
<221>	CDS			
<222>	(21)..(254)			
<400>	127			
gaattcgcgcc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg				
				53

Met Gln Thr Ala Tyr Trp Val Met Val Met Met
1 5 10

atg gtg tgg att aca gcc cct ctg tct gaa ggt gat aaa ttg aac gac 101
Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Asp Lys Leu Asn Asp
15 20 25

gta att cgg ggt ttg gtg cca gat aac tta gcc cca cag ctt gtt ttg 149
Val Ile Arg Gly Leu Val Pro Asp Asn Leu Ala Pro Gln Leu Val Leu
30 35 40

caa agt ctg gat tcc cgt cgt cat cct cac ggc att cgt cag gat gga 197
Gln Ser Leu Asp Ser Arg Arg His Pro His Gly Ile Arg Gln Asp Gly
45 50 55

gcc caa ata tgt atc tgg aag ata tgt cca cca tcc cca tgg aaa cga 245
Ala Gln Ile Cys Ile Trp Lys Ile Cys Pro Pro Ser Pro Trp Lys Arg
60 65 70 75

ctt gga tct taagaaaaga aacaattgac gtcagacaac cgccacaact 294
Leu Gly Ser

tgagtacgac atcgtaata caacttcagc aaatatgaaa ttttcagcat cactgtgggt 354

gtgaagaaat cagttgcttt aaaggattgg atttgcctt gttaagagt tgtactgatg 414

tcatctctgc actatgaaat aaagctgatg tgacaagcaa aaaaaaaaaa aaaaaagtac 474

tetgcgttgt tactcgagct taagggcgaa ttc 507

<210> 128
<211> 78
<212> PRT
<213> Conus litoglyphus

<400> 128
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
1 5 10 15
Ala Pro Leu Ser Glu Gly Asp Lys Leu Asn Asp Val Ile Arg Gly Leu
20 25 30
Val Pro Asp Asn Leu Ala Pro Gln Leu Val Leu Gln Ser Leu Asp Ser
35 40 45
Arg Arg His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile
50 55 60
Trp Lys Ile Cys Pro Pro Ser Pro Trp Lys Arg Leu Gly Ser
65 70 75

<210> 129
<211> 28
<212> PRT
<213> Conus litoglyphus

<220>
<221> PEPTIDE
<222> (1)..(28)
<223> Xaa at residues 2, 19, 20 and 22 may be Pro or hydroxy-Pro; Xaa a
t residues 15 and 23 may be Trp (D or L) or bromo-Trp (D or L)

<400> 129

His Xaa His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile Xaa Lys
1 5 10 15

Ile Cys Xaa Xaa Ser Xaa Xaa Lys Arg Leu Gly Ser
20 25

<210> 130
<211> 507
<212> DNA
<213> Conus litteratus

<220>
<221> CDS
<222> (21)..(299)

<400> 130
gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53
Met Gln Thr Ala Tyr Trp Val Met Val Met Met
1 5 10

atg gtg ggg att aca gcc cct ctg tct gaa ggt cgt aaa ttg aac gac 101
Met Val Gly Ile Thr Ala Pro Leu Ser Glu Gly Arg Lys Leu Asn Asp
15 20 25

gca att cgg ggt ttg gtg cca gat gac tta acc cca cag ctt ttg cga 149
Ala Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Pro Gln Leu Leu Arg
30 35 40

agt ccg gtt tcg act cct tat cct gag ttt cat ctt gat gaa cct tat 197
Ser Pro Val Ser Thr Pro Tyr Pro Glu Phe His Leu Asp Glu Pro Tyr
45 50 55

ctg aag ata ccc gta tgt atc tgg aag ata tgt cca cca aac cta ttg 245
Leu Lys Ile Pro Val Cys Ile Trp Lys Ile Cys Pro Pro Asn Leu Leu
60 65 70 75

aga cga cgt gat ctt aag aaa aga aac aaa gta cgt cag aca acc gcc 293
Arg Arg Arg Asp Leu Lys Lys Arg Asn Lys Val Arg Gln Thr Thr Ala
80 85 90

aca act tgagtacgac atcggttcata caacttgagc aaatatttca gcatcactat 349
Thr Thr

ggttgtgaag aaatcagttg ctttaaaaga ttggatcttt cttgttttaa gagttgtatt 409

gatgtcagct ctgcactctg aaataaagct gatgtgacaa acaaaaaaaaa aaaaaaaaaa 469

agtactctgc gttgttactc gagcttaagg gcgaattc 507

<210> 131
<211> 93
<212> PRT
<213> Conus litteratus

<400> 131
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Gly Ile Thr
1 5 10 15

Ala Pro Leu Ser Glu Gly Arg Lys Leu Asn Asp Ala Ile Arg Gly Leu
20 25 30

Val Pro Asp Asp Leu Thr Pro Gln Leu Leu Arg Ser Pro Val Ser Thr
35 40 45

Pro Tyr Pro Glu Phe His Leu Asp Glu Pro Tyr Leu Lys Ile Pro Val
50 55 60

Cys Ile Trp Lys Ile Cys Pro Pro Asn Leu Leu Arg Arg Arg Asp Leu
65 70 75 80

Lys Lys Arg Asn Lys Val Arg Gln Thr Thr Ala Thr Thr
85 90

<210> 132
<211> 50
<212> PRT
<213> Conus litteratus

<220>
<221> PEPTIDE
<222> (1)..(50)
<223> Xaa at residues 2, 6, 8, 15, 20, 28 and 29 may be Pro or hydroxy-Pro; Xaa at residues 7 and 16 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 9 and 14 may be Glu or Gla

<220>
<221> PEPTIDE
<222> (1)..(50)
<223> Xaa at residue 24 may be Trp (D or L) or bromo-Trp (D or L)

<400> 132
Ser Xaa Val Ser Thr Xaa Xaa Xaa Xaa Phe His Leu Asp Xaa Xaa Xaa
1 5 10 15

Leu Lys Ile Xaa Val Cys Ile Xaa Lys Ile Cys Xaa Xaa Asn Leu Leu
20 25 30

Arg Arg Arg Asp Leu Lys Lys Arg Asn Lys Val Arg Gln Thr Thr Ala
35 40 45

Thr Thr
50

<210> 133
<211> 508
<212> DNA
<213> Conus litteratus

<220>
<221> CDS
<222> (21)..(275)

<400> 133
gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53
Met Gln Thr Ala Tyr Trp Val Met Val Met Met
1 5 10

atg gtg ggg att aca gcc cct ctg tct gaa ggt cgt aaa ttg aac gac 101
Met Val Gly Ile Thr Ala Pro Leu Ser Glu Gly Arg Lys Leu Asn Asp
15 20 25

gca att cgg ggt ttg gtg cca aat gac tta acc cca cag ctt ttg caa 149
Ala Ile Arg Gly Leu Val Pro Asn Asp Leu Thr Pro Gln Leu Leu Gln
30 35 40

agt ctg gtt tcc cgt cgt cat cgt gtg ttt cat ctt gac aac act tat 197

Ser Leu Val Ser Arg Arg His Arg Val Phe His Leu Asp Asn Thr Tyr
 45 50 55
 ctc aag ata ccc ata tgt gcc tgg aag gta tgt cca cca acc cca tgg 245
 Leu Lys Ile Pro Ile Cys Ala Trp Lys Val Cys Pro Pro Thr Pro Trp
 60 65 70 75
 aga cga cgt gat ctt aag aaa aga aac aaa tgacgtcaga caaccgccac 295
 Arg Arg Arg Asp Leu Lys Lys Arg Asn Lys
 80 85
 aacttgagta cgacattgtt aatgcgactt gagcaaattt ttcagcatca ctatggttgt 355
 aaagaaatca gctgctttaa acgattggat ctttccttat ttaagagttg tattgatgtc 415
 agctctgcac tctgaaataa agctgatgtg acaaacaaaa aaaaaaaaaa aaaaaagtac 475
 tctgcgttgt tactcgagct taagggcgaa ttc 508

<210> 134
 <211> 85
 <212> PRT
 <213> Conus litteratus

<400> 134
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Gly Ile Thr
 1 5 10 15
 Ala Pro Leu Ser Glu Gly Arg Lys Leu Asn Asp Ala Ile Arg Gly Leu
 20 25 30
 Val Pro Asn Asp Leu Thr Pro Gln Leu Leu Gln Ser Leu Val Ser Arg
 35 40 45
 Arg His Arg Val Phe His Leu Asp Asn Thr Tyr Leu Lys Ile Pro Ile
 50 55 60
 Cys Ala Trp Lys Val Cys Pro Pro Thr Pro Trp Arg Arg Arg Asp Leu
 65 70 75 80
 Lys Lys Arg Asn Lys
 85

<210> 135
 <211> 36
 <212> PRT
 <213> Conus litteratus

<220>
 <221> PEPTIDE
 <222> (1)..(36)
 <223> Xaa at residue 10 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 14, 22, 23 and
 25 may be Pro or hydroxy-Pro; Xaa at residues 18 and 26 may be Trp
 (D or L) or bromo-Trp (D or L)

<400> 135
 His Arg Val Phe His Leu Asp Asn Thr Xaa Leu Lys Ile Xaa Ile Cys
 1 5 10 15
 Ala Xaa Lys Val Cys Xaa Xaa Thr Xaa Xaa Arg Arg Arg Asp Leu Lys
 20 25 30
 Lys Arg Asn Lys
 35

```
<220>
<221> CDS
<222> (21)..(236)
<220>
<221> misc_feature
<222> (1)..(498)
<223> n may be any base
```

atg gtg tgg att aaa ggc cct gtg tct gaa ggt ggt aaa ttg aac gac 101
Met Val Trp Ile Lys Gly Pro Val Ser Glu Gly Gly Lys Leu Asn Asp
15 20 25

gta att cgg ggt ttg gtg cca gac gac tta acc cca cag ctt atc ttg 149
Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu
30 35 40

caa agt ctg atg tcc cgt cgt cgt tct gac agc gat gtt cgg gag gtg 197
Gln Ser Leu Met Ser Arg Arg Arg Ser Asp Ser Asp Val Arg Glu Val
45 50 55

tac ata tta tgc atc tgg aag ata tgt cca cca ttg cca tgaagacgac 246
 Tyr Ile Leu Cys Ile Trp Lys Ile Cys Pro Pro Leu Pro
 60 65 70

atgatcttaa ggaaaaagqat aaacgacgtc agacaaccgc tacaactgta gtacgacatc 306

gttaatacga cttcagcaaa tatttgaaca tcaactgtggt tgtgaagaaa tcagttgctt 366

taaacgattg gatttttcct taagagttgc actgatatca gctctgcact atgaaataaa 426

gctgatgtga ctaccaaaaa aaaaaaaaaa aaaaagtact ntgcgttggt actcgagctt 486

aagggcgaat tc 498

```
<210> 137
<211> 72
<212> PRT
<213> Conus loroisii
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```
<400> 137
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Lys
1          5          10          15
```

Gly Pro Val Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
20 25 30

Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Gln Ser Leu Met Ser
35 40 45

Arg Arg Arg Ser Asp Ser Asp Val Arg Glu Val Tyr Ile Leu Cys Ile
50 55 60

Trp Lys Ile Cys Pro Pro Leu Pro

65

70

<210> 138
 <211> 22
 <212> PRT
 <213> *Conus loroisii*
 <220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 8 may be Glu or Gla; Xaa at residue 10 may be Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-
 Tyr; Xaa at residue 15 may be Trp (D or L) or bromo-Trp (D or L);
 Xaa at residues 19, 20 and 22 may be Pro or hydroxy-Pro

<400> 138
 Arg Ser Asp Ser Asp Val Arg Xaa Val Xaa Ile Leu Cys Ile Xaa Lys
 1 5 10 15

Ile Cys Xaa Xaa Leu Xaa
 20

<210> 139
 <211> 495
 <212> DNA
 <213> *Conus magus*

<220>
 <221> CDS
 <222> (21)..(242)

<400> 139
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met
 1 5 10

atg gtg tgg att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac 101
 Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp
 15 20 25

gta att cgg ggt ttg gtg cca cac tcc tta acc cca cag cat atc ttg 149
 Val Ile Arg Gly Leu Val Pro His Ser Leu Thr Pro Gln His Ile Leu
 30 35 40

caa agt ctg act tcc cgt aat ggt tct ggc agc agc aat cag aaa gaa 197
 Gln Ser Leu Thr Ser Arg Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu
 45 50 55

gca caa cta tgc atc tgg aag gta tgt cca cca tcc cca tgg aga 242
 Ala Gln Leu Cys Ile Trp Lys Val Cys Pro Pro Ser Pro Trp Arg
 60 65 70

tgaccacaag gaaaaagatg aacggcgtca gacaaccgcc acaactgtag tgggacatcg 302

ttgatacgac ttcaacaaat attttaacat cactgtgggt gttaaagaaat cagttgcttt 362

aaaagattgg atttttcctt gtttaagagt tgtactgata tcagctctgc actatgaaat 422

aaagctgatg tgacaaacaa aaaaaaaaaa aaaaaagtac tctgcgttgt tactcgagct 482

taagggcgaa ttc 495

<210> 140
 <211> 74
 <212> PRT

<213> Conus magus

<400> 140

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
20 25 30

Val Pro His Ser Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser
35 40 45

Arg Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu Ala Gln Leu Cys Ile
50 55 60

Trp Lys Val Cys Pro Pro Ser Pro Trp Arg
65 70

<210> 141

<211> 25

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 10 may be Glu or Gla; Xaa at residues 16 and 24 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 20, 21 and 23 may be Pro or hydroxy-Pro

<400> 141

Asn Gly Ser Gly Ser Ser Asn Gln Lys Xaa Ala Gln Leu Cys Ile Xaa
1 5 10 15

Lys Val Cys Xaa Xaa Ser Xaa Xaa Arg
20 25

<210> 142

<211> 587

<212> DNA

<213> Conus miles

<220>

<221> CDS

<222> (21)..(347)

<220>

<221> misc_feature

<222> (1)..(587)

<223> n may be any nucleotide

<400> 142

gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg atg atg gtg 53
Met Gln Thr Ala Tyr Trp Val Met Met Met Val
1 5 10

gtg atg atg gtg ggg gtt act gtc gct ggc tcc ctg cct gtg ttt gat 101
Val Met Met Val Gly Val Thr Val Ala Gly Ser Leu Pro Val Phe Asp
15 20 25

gac gac aac gac tct gac ccc gct gtc aag cgc gct atc acg tgg tcc 149
Asp Asp Asn Asp Ser Asp Pro Ala Val Lys Arg Ala Ile Thr Trp Ser
30 35 40

cgc atc ctg ggc gtg tct cca gcc ttc ctg gca cag cag cga gcg ctg 197
 Arg Ile Leu Gly Val Ser Pro Ala Phe Leu Ala Gln Gln Arg Ala Leu
 45 50 55

gtt ccc ttc gcc aac cga ttc atc agt gag cag aaa cgt ttc cga ccc 245
 Val Pro Phe Ala Asn Arg Phe Ile Ser Glu Gln Lys Arg Phe Arg Pro
 60 65 70 75

gcc atg cag agc cga tca gga gga atg tcg ctg tgc cta tgg aaa gtg 293
 Ala Met Gln Ser Arg Ser Gly Gly Met Ser Leu Cys Leu Trp Lys Val
 80 85 90

tgt cct gca gcc ccc tgg ctg gtc gcc aaa cgt aaa cag gaa acc agc 341
 Cys Pro Ala Ala Pro Trp Leu Val Ala Lys Arg Lys Gln Glu Thr Ser
 95 100 105

gac tac tgacgtcata cctctaaaga ccactcatg acgtcaacgc tgaactgacg 397
 Asp Tyr

tcaccgacag ctccaacgtc acagcaggag cgagagagag gctggagcat ttctctttct 457

tttggttttt cgagttgaag tgtgatcagc tgggctggtg aaaaaattgt tgagtaaagt 517

tgaatgaaaa tcaaaaaaaaa aaaaaaaaaa agtactctgc gttggtactc gaggcttaaa 577

ggcgnaattc 587

<210> 143

<211> 109

<212> PRT

<213> Conus miles

<400> 143

Met Gln Thr Ala Tyr Trp Val Met Met Met Val Val Met Met Val Gly
 1 5 10 15

Val Thr Val Ala Gly Ser Leu Pro Val Phe Asp Asp Asp Asn Asp Ser
 20 25 30

Asp Pro Ala Val Lys Arg Ala Ile Thr Trp Ser Arg Ile Leu Gly Val
 35 40 45

Ser Pro Ala Phe Leu Ala Gln Gln Arg Ala Leu Val Pro Phe Ala Asn
 50 55 60

Arg Phe Ile Ser Glu Gln Lys Arg Phe Arg Pro Ala Met Gln Ser Arg
 65 70 75 80

Ser Gly Gly Met Ser Leu Cys Leu Trp Lys Val Cys Pro Ala Ala Pro
 85 90 95

Trp Leu Val Ala Lys Arg Lys Gln Glu Thr Ser Asp Tyr
 100 105

<210> 144

<211> 37

<212> PRT

<213> Conus miles

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residues 3, 21 and 24 may be Pro or hydroxy-Pro; Xaa at re

sidues 17 and 25 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residue 33 may be Glu or Gla;

<220>
 <221> PEPTIDE
 <222> (1)..(37)
 <223> Xaa at residue 37 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 144
 Phe Arg Xaa Ala Met Gln Ser Arg Ser Gly Gly Met Ser Leu Cys Leu
 1 5 10 15
 Xaa Lys Val Cys Xaa Ala Ala Xaa Xaa Leu Val Ala Lys Arg Lys Gln
 20 25 30
 Xaa Thr Ser Asp Xaa
 35

<210> 145
 <211> 499
 <212> DNA
 <213> Conus miles

<220>
 <221> CDS
 <222> (21)..(401)

<400> 145
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met
 1 5 10
 atg gtg gtg ggt tca ccg tcc gga gtc acg tcc atc ggt ctc aca gtc 101
 Met Val Val Gly Ser Pro Ser Gly Val Thr Ser Ile Gly Leu Thr Val
 15 20 25
 cta cgt cgc gca acc atg gtg atg act cca ttc atg aca aga cga ttc 149
 Leu Arg Arg Ala Thr Met Val Met Thr Pro Phe Met Thr Arg Arg Phe
 30 35 40
 atc aac atc tgt ttg ccc gtc ttc ctc tgg aga aca acg acg acc atc 197
 Ile Asn Ile Cys Leu Pro Val Phe Leu Trp Arg Thr Thr Thr Thr Ile
 45 50 55
 gtt ctg tgg atc ttc ctg cag tgt atg cgc cgg gcc agg cac gtg tgc 245
 Val Leu Trp Ile Phe Leu Gln Cys Met Arg Arg Ala Arg His Val Cys
 60 65 70 75
 gtt cta ctt ttg ttc ttg acc tca ttg cag ata ggg gtt ggt gca gac 293
 Val Leu Leu Leu Phe Leu Thr Ser Leu Gln Ile Gly Val Gly Ala Asp
 80 85 90
 gac atg aaa cta cag cgc caa aga cgt caa ggt ttc tgt tgc gtc gtt 341
 Asp Met Lys Leu Gln Arg Gln Arg Arg Gln Gly Phe Cys Cys Val Val
 95 100 105
 atc ccg att ctt tgg ttc tgt tgt ggg ggt tac cgc aca aat ggc act 389
 Ile Pro Ile Leu Trp Phe Cys Cys Gly Gly Tyr Arg Thr Asn Gly Thr
 110 115 120
 gca ctg gcc gat tgaaagaact gcaataaacg gaatggcaag aaggaataaa 441
 Ala Leu Ala Asp
 125

aaaaaaaaa aaaaaaaaaa agtactctgc gttgttactc gagcttaagg gcgaattc 499

<210> 146
 <211> 127
 <212> PRT
 <213> Conus miles

<400> 146
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Gly Ser
 1 5 10 15
 Pro Ser Gly Val Thr Ser Ile Gly Leu Thr Val Leu Arg Arg Ala Thr
 20 25 30
 Met Val Met Thr Pro Phe Met Thr Arg Arg Phe Ile Asn Ile Cys Leu
 35 40 45
 Pro Val Phe Leu Trp Arg Thr Thr Thr Thr Ile Val Leu Trp Ile Phe
 50 55 60
 Leu Gln Cys Met Arg Arg Ala Arg His Val Cys Val Leu Leu Leu Phe
 65 70 75 80
 Leu Thr Ser Leu Gln Ile Gly Val Gly Ala Asp Asp Met Lys Leu Gln
 85 90 95
 Arg Gln Arg Arg Gln Gly Phe Cys Cys Val Val Ile Pro Ile Leu Trp
 100 105 110
 Phe Cys Cys Gly Gly Tyr Arg Thr Asn Gly Thr Ala Leu Ala Asp
 115 120 125

<210> 147
 <211> 27
 <212> PRT
 <213> Conus miles

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 9 may be Pro
 or hydroxy-Pro; Xaa at residue 12 may be Trp (D or L) or bromo-Trp
 p(D or L); Xaa at residue 18 may be Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 147
 Xaa Gly Phe Cys Cys Val Val Ile Xaa Ile Leu Xaa Phe Cys Cys Gly
 1 5 10 15
 Gly Xaa Arg Thr Asn Gly Thr Ala Leu Ala Asp
 20 25

<210> 148
 <211> 450
 <212> DNA
 <213> Conus muriculatus

<220>
 <221> CDS
 <222> (1)..(237)

<400> 148
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg tgg att aca

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
1 5 10 15

gcc cct ttg tct gaa ggt ggt aaa ctg aac gat gta att cgg ggt ttc 96
Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Phe
20 25 30

gcg cta gat gac tta gcc caa agc cgt att atg caa agt ctg gtt ttc 144
Ala Leu Asp Asp Leu Ala Gln Ser Arg Ile Met Gln Ser Leu Val Phe
35 40 45

agt cat cag cct ctt cca acg gca tcc ata tgt atc tgg aag ata tgt 192
Ser His Gln Pro Leu Pro Thr Ala Ser Ile Cys Ile Trp Lys Ile Cys
50 55 60

cca cca gac cca tgg aga cga cat gat ctt cag aaa agt aac aaa 237
Pro Pro Asp Pro Trp Arg Arg His Asp Leu Gln Lys Ser Asn Lys
65 70 75

tgacgtcaga caaccgccac aacttgaata caacatcatt aatacgactt cagcaaatat 297

tttaacatca ctgtgattgt tcggaagtca gttgctttaa aggattggat ttgtccctgt 357

tgtattgatg tcaactctgc actatgaaat aaagctgatg tgacaaacaa gaaaaaaaaa 417

aaaaaaaaaa agtactctgc gttgttactc gag 450

<210> 149
<211> 79
<212> PRT
<213> Conus muriculatus

<400> 149
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Phe
20 25 30

Ala Leu Asp Asp Leu Ala Gln Ser Arg Ile Met Gln Ser Leu Val Phe
35 40 45

Ser His Gln Pro Leu Pro Thr Ala Ser Ile Cys Ile Trp Lys Ile Cys
50 55 60

Pro Pro Asp Pro Trp Arg Arg His Asp Leu Gln Lys Ser Asn Lys
65 70 75

<210> 150
<211> 38
<212> PRT
<213> Conus muriculatus
<220>
<221> PEPTIDE
<222> (1)..(38)
<223> Xaa at residues 11, 13, 24, 25 and 27 may be Pro or hydroxy-Pro;
Xaa at residue 20 and 28 may be Trp or bromo-Trp

<400> 150
Ile Met Gln Ser Leu Val Phe Ser His Gln Xaa Leu Xaa Thr Ala Ser
1 5 10 15

Ile Cys Ile Xaa Lys Ile Cys Xaa Xaa Asp Xaa Xaa Arg Arg His Asp
20 25 30

<210> 153

$\langle 210 \rangle$	155
$\langle 211 \rangle$	72

<212> PRT
 <213> Conus musicus

<400> 155
 Met Gln Thr Ala Tyr Trp Val Met Met Met Met Met Met Val Trp Met
 1 5 10 15
 Thr Ala Pro Leu Ser Glu Gly Arg Lys Leu Ile Asp Lys Val Arg Gly
 20 25 30
 Met Gly Pro Gly Asp Leu Ser Leu Gln Lys Met Phe Pro Ser Leu Ala
 35 40 45
 Leu Gly Pro Gly Gly Asp Val Ile Cys Arg Trp Lys Val Cys Pro Pro
 50 55 60
 Thr Pro Trp Lys Arg Leu Ile Lys
 65 70

<210> 156
 <211> 41
 <212> PRT
 <213> Conus musicus

<220>
 <221> PEPTIDE
 <222> (1)..(41)
 <223> Xaa at residues 4, 14, 20, 32, 33 and 35 may be Pro or hydroxy-Pro;
 Xaa at residues 28 and 36 may be Trp (D or L) or bromo-Trp (D or L).

<400> 156
 Gly Met Gly Xaa Gly Asp Leu Ser Leu Gln Lys Met Phe Xaa Ser Leu
 1 5 10 15
 Ala Leu Gly Xaa Gly Gly Asp Val Ile Cys Arg Xaa Lys Val Cys Xaa
 20 25 30
 Xaa Thr Xaa Xaa Lys Arg Leu Ile Lys
 35 40

<210> 157
 <211> 449
 <212> DNA
 <213> Conus musicus

<220>
 <221> CDS
 <222> (1)..(243)

<400> 157
 atg cag acg gcc tac tgg gtg atg atg atg atg acg atg atg gtg tgg 48
 Met Gln Thr Ala Tyr Trp Val Met Met Met Met Thr Met Met Val Trp
 1 5 10 15
 atg aca gcc cct ctg tct gaa ggt cgt cca ctg agc gac aaa gtt cgg 96
 Met Thr Ala Pro Leu Ser Glu Gly Arg Pro Leu Ser Asp Lys Val Arg
 20 25 30
 ggt atg gtg cca ggc gac tta gcc ctg cag tat ctg ttc cca agt ctg 144
 Gly Met Val Pro Gly Asp Leu Ala Leu Gln Tyr Leu Phe Pro Ser Leu
 35 40 45
 gct ttc aat ccc ccg gac ata tgt acg tgg aag gta tgt cca cca ccc 192

Ala Phe Asn Pro Pro Asp Ile Cys Thr Trp Lys Val Cys Pro Pro Pro
50 55 60

cca tgg aga cga cca aaa aaa ata act gac gtc gga cag ccg cca caa 240
Pro Trp Arg Arg Pro Lys Lys Ile Thr Asp Val Gly Gln Pro Pro Gln
65 70 75 80

ctg tagtacgaca tcgttgatac gacttcagca aatattttca acatcactgc 293
Leu

ggttgtgaag aaatcagttg ttttaaaagg ttggattttt ccttgtttaa aagagctgta 353

ctgatgtcag ctctgcatta cgaaataaag ctgatgtgac aaacgaaaaa aaaaaaaaaa 413

aaaaaaaaaa aaaagtactc tgcgttggtta ctcgag 449

<210> 158
<211> 81
<212> PRT
<213> Conus musicus

<400> 158
Met Gln Thr Ala Tyr Trp Val Met Met Met Met Thr Met Met Val Trp
1 5 10 15

Met Thr Ala Pro Leu Ser Glu Gly Arg Pro Leu Ser Asp Lys Val Arg
20 25 30

Gly Met Val Pro Gly Asp Leu Ala Leu Gln Tyr Leu Phe Pro Ser Leu
35 40 45

Ala Phe Asn Pro Pro Asp Ile Cys Thr Trp Lys Val Cys Pro Pro Pro
50 55 60

Pro Trp Arg Arg Pro Lys Lys Ile Thr Asp Val Gly Gln Pro Pro Gln
65 70 75 80

Leu

<210> 159
<211> 49
<212> PRT
<213> Conus musicus

<220>
<221> PEPTIDE
<222> (1)..(49)
<223> Xaa at residues 4, 14, 20, 21, 30, 31, 32, 33, 37, 46 and 47 may
be Pro or hydroxy-Pro; Xaa at residue 11 may be Tyr, 125I-Tyr, mo
no-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at r
esidues 26 and 34 may be Trp (D or L) or bromo-Trp (D or L)

<400> 159
Gly Met Val Xaa Gly Asp Leu Ala Leu Gln Xaa Leu Phe Xaa Ser Leu
1 5 10 15

Ala Phe Asn Xaa Xaa Asp Ile Cys Thr Xaa Lys Val Cys Xaa Xaa Xaa
20 25 30

Xaa Xaa Arg Arg Xaa Lys Lys Ile Thr Asp Val Gly Gln Xaa Xaa Gln
35 40 45

Leu

<210> 160
 <211> 436
 <212> DNA
 <213> Conus musicus

<220>
 <221> CDS
 <222> (1)..(240)

<400> 160
 atg cag acg gcc tac tgg gtg atg atg atg acg atg atg gtg tgg atg 48
 Met Gln Thr Ala Tyr Trp Val Met Met Met Thr Met Met Val Trp Met
 1 5 10 15
 aca gcc cct ctg tct gaa ggt cgt cca ctg agc gac aaa gtt cgg ggt 96
 Thr Ala Pro Leu Ser Glu Gly Arg Pro Leu Ser Asp Lys Val Arg Gly
 20 25 30
 atg gtg cca ggc gac tta gtc ctg cag tat ctg ttc cca agt ctg gct 144
 Met Val Pro Gly Asp Leu Val Leu Gln Tyr Leu Phe Pro Ser Leu Ala
 35 40 45
 ttc aat cct ccg gac ata tgt acg tgg aag gta tgt cca cca ccc cca 192
 Phe Asn Pro Pro Asp Ile Cys Thr Trp Lys Val Cys Pro Pro Pro Pro
 50 55 60
 tgg aga cga cca aaa aaa ata act gac gtc aga cag ccg cca caa ctg 240
 Trp Arg Arg Pro Lys Lys Ile Thr Asp Val Arg Gln Pro Pro Gln Leu
 65 70 75 80
 tagtacgaca tcgttgatac gacttcagca aatattttca acatcactgc ggttgtgaag 300
 aaatcagttg ttttaaaagg ttggattttt ccttgtttaa aagagctgta ctgatgtcag 360
 ctctgcatta cgaaataaag ctgatgtgac aagcaaaaaa aaaaaaaaaa aaaagtactc 420
 tgcgttggtta ctcgag 436

<210> 161
 <211> 80
 <212> PRT
 <213> Conus musicus

<400> 161
 Met Gln Thr Ala Tyr Trp Val Met Met Met Thr Met Met Val Trp Met
 1 5 10 15
 Thr Ala Pro Leu Ser Glu Gly Arg Pro Leu Ser Asp Lys Val Arg Gly
 20 25 30
 Met Val Pro Gly Asp Leu Val Leu Gln Tyr Leu Phe Pro Ser Leu Ala
 35 40 45
 Phe Asn Pro Pro Asp Ile Cys Thr Trp Lys Val Cys Pro Pro Pro Pro
 50 55 60
 Trp Arg Arg Pro Lys Lys Ile Thr Asp Val Arg Gln Pro Pro Gln Leu
 65 70 75 80

<210> 162
 <211> 49
 <212> PRT
 <213> Conus musicus

<220>
 <221> PEPTIDE
 <222> (1)..(49)
 <223> Xaa at residues 4, 14, 20, 21, 30, 31, 32, 33, 37, 46 and 47 may be Pro or hydroxy-Pro; Xaa at residue 11 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 26 and 34 may be Trp (D or L) or bromo-Trp (D or L)

<400> 162
 Gly Met Val Xaa Gly Asp Leu Val Leu Gln Xaa Leu Phe Xaa Ser Leu
 1 5 10 15
 Ala Phe Asn Xaa Xaa Asp Ile Cys Thr Xaa Lys Val Cys Xaa Xaa Xaa
 20 25 30
 Xaa Xaa Arg Arg Xaa Lys Lys Ile Thr Asp Val Arg Gln Xaa Xaa Gln
 35 40 45

Leu

<210> 163
 <211> 462
 <212> DNA
 <213> Conus mustelinus

<220>
 <221> CDS
 <222> (1)..(225)

<400> 163
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gcg tgg tat aca 48
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Ala Trp Tyr Thr
 1 5 10 15
 acc cct gtg tct gaa tgt ggg aaa ttg aac aac gta att cgg ggt ttt 96
 Thr Pro Val Ser Glu Cys Gly Lys Leu Asn Asn Val Ile Arg Gly Phe
 20 25 30
 gtg cca aag gac tgg acc cca atg ctt ccc tgg cgt cgt cta gtt tcc 144
 Val Pro Lys Asp Trp Thr Pro Met Leu Pro Trp Arg Arg Leu Val Ser
 35 40 45
 cat acc agc agc aag tat cca ggt gtg act ttt tgt cca tgg aag gtg 192
 His Thr Ser Ser Lys Tyr Pro Gly Val Thr Phe Cys Pro Trp Lys Val
 50 55 60
 tgt ccg cca gcg cca tgg aga ata ctt ggg gtc taacgcaaaa aaatacatga 245
 Cys Pro Pro Ala Pro Trp Arg Ile Leu Gly Val
 65 70 75
 cgtcagacaa ccgccaccgc tttagtagca catcggtcat acgtctccag caagtatttt 305
 aacatcactg tgggtgtgaa gaagtcagta gctttaaaag attggatttt ttccttgttt 365
 aagagttgta ctgacatgag ttctgcacta tgaaataaag ttgatgtgac gaacgaaaaa 425
 aaaaaaaaaa aaaaagtact ctgcgttggtt actcgag 462

<210> 164
 <211> 75
 <212> PRT
 <213> Conus mustelinus

<400> 164

ctg gct ccc ttc gcc aac cga ccc atc aat gag cag aaa cgt ttc cga 245
Leu Ala Pro Phe Ala Asn Arg Pro Ile Asn Glu Gln Lys Arg Phe Arg
60 65 70 75

cct gcc gtg aag agc cga tca cga cga gcg ccg ccg tgc gtg tgg aag 293
Pro Ala Val Lys Ser Arg Ser Arg Arg Ala Pro Pro Cys Val Trp Lys
80 85 90

gtg tgt ccc gct ccc ccc tgg ctg gtc acc aaa cgt aaa cag gaa acc 341
Val Cys Pro Ala Pro Pro Trp Leu Val Thr Lys Arg Lys Gln Glu Thr
95 100 105

agc gac tac tgacgtcata cctcaataga ccgactcatg acttcaacgc 390
Ser Asp Tyr
110

tgaattgacg tcaccgagag ctccaacgtc acagcaggag cgagagagag agagagagag 450

agagaaagag agagagaaag gctggagtat ttctctttct tttgggtttt cgtgttgaag 510

tgtgatcagc tgggctggtt caaaattggt gaataaagtt gaatgaaaat caaaaaaaaa 570

aaaaaaaaaa aagtactctg cgttgttact cgagcttaag ggcgaattc 619

<210> 167

<211> 110

<212> PRT

<213> Conus nobilis

<400> 167

Met Gln Thr Ala Tyr Trp Val Met Met Met Val Val Val Met Met Val
1 5 10 15
Gly Val Thr Val Ala Gly Ser Leu Ser Val Phe Asp Asp Asp Asn Asp
20 25 30

Ser Asp Pro Ala Val Lys Arg Ala Ile Thr Trp Ser Arg Phe Leu Gly
35 40 45

Ala Ser Pro Ala Phe Leu Ala Gln Gln Arg Ala Leu Ala Pro Phe Ala
50 55 60

Asn Arg Pro Ile Asn Glu Gln Lys Arg Phe Arg Pro Ala Val Lys Ser
65 70 75 80

Arg Ser Arg Arg Ala Pro Pro Cys Val Trp Lys Val Cys Pro Ala Pro
85 90 95

Pro Trp Leu Val Thr Lys Arg Lys Gln Glu Thr Ser Asp Tyr
100 105 110

<210> 168

<211> 37

<212> PRT

<213> Conus nobilis

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residues 3, 13, 14, 21, 23 and 24 may be Pro or hydroxy-Pr
o; Xaa at residues 17 and 25 may be Trp (D or L) or bromo-Trp (D
or L); Xaa at residue 33 may be Glu or Gla;

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residue 37 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty
r, O-sulpho-Tyr or O-phospho-Tyr

<400> 168

Phe Arg Xaa Ala Val Lys Ser Arg Ser Arg Arg Ala Xaa Xaa Cys Val
 1 5 10 15

Xaa Lys Val Cys Xaa Ala Xaa Xaa Xaa Leu Val Thr Lys Arg Lys Gln
 20 25 30

Xaa Thr Ser Asp Xaa
 35

<210> 169

<211> 494

<212> DNA

<213> Conus nobilis

<220>

<221> CDS

<222> (21)..(242)

<400> 169

gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met
 1 5 10

atg gtg tgg att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac 101
 Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp
 15 20 25

gta att cgg ggt ttg gtg cca cac ttc tta acc cca cag cat atc ttg 149
 Val Ile Arg Gly Leu Val Pro His Phe Leu Thr Pro Gln His Ile Leu
 30 35 40

caa agt ctg act tcc cgt aat ggt tct ggc agc agt aat cag aaa gaa 197
 Gln Ser Leu Thr Ser Arg Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu
 45 50 55

gcg caa cta tgc atc tgg aag gta tgt cca cca acc cca tgg aga 242
 Ala Gln Leu Cys Ile Trp Lys Val Cys Pro Thr Pro Trp Arg
 60 65 70

tgatcacaag gaaaaagatg aacggcgtca gacaaccgcc acaactgtag tgggacatcg 302

ttgatacgac ttcagcaaatt attttaacat cactgtgggt gtgaagaaat cagttgtttt 362

aaaagattgg atttttcctt gtttaagagt tgtactgata tcagctctgc actatgaaat 422

aaagctgatg tgacaagcaa aaaaaaaaaa aaaaagtact ctgcgttggt actcgagctt 482

aagggcgaat tc 494

<210> 170

<211> 74

<212> PRT

<213> Conus nobilis

<400> 170

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
 1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30

Val Pro His Phe Leu Thr Pro Gln His Ile Leu Gln Ser Leu Thr Ser
 35 40 45

Arg Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu Ala Gln Leu Cys Ile
 50 55 60

Trp Lys Val Cys Pro Pro Thr Pro Trp Arg
 65 70

<210> 171
 <211> 25
 <212> PRT
 <213> Conus nobilis

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 10 may be Glu or Glu; Xaa at residues 16 and 24 may be Trp or bromo-Trp; Xaa at residues 20, 21 and 23 may be Pro or hydroxy-Pro

<400> 171
 Asn Gly Ser Gly Ser Ser Asn Gln Lys Xaa Ala Gln Leu Cys Ile Xaa
 1 5 10 15

Lys Val Cys Xaa Xaa Thr Xaa Xaa Arg
 20 25

<210> 172
 <211> 604
 <212> DNA
 <213> Conus nobilis

<220>
 <221> CDS
 <222> (21)..(350)

<400> 172
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg atg atg gtg 53
 Met Gln Thr Ala Tyr Trp Val Met Met Met Val
 1 5 10

gtg gtg atg atg gtg ggg gtt act gtc gct ggc tca ctg tct gtg ttt 101
 Val Val Met Met Val Gly Val Thr Val Ala Gly Ser Leu Ser Val Phe
 15 20 25

gat gac gac aat gac tct gac cca gct gtc aag cgc gcc atc acg tgg 149
 Asp Asp Asp Asn Asp Ser Asp Pro Ala Val Lys Arg Ala Ile Thr Trp
 30 35 40

tct cga ttc ctg ggc gcg tct cca gcc ttc ctg gca cag cag cga gcg 197
 Ser Arg Phe Leu Gly Ala Ser Pro Ala Phe Leu Ala Gln Gln Arg Ala
 45 50 55

ctg gct ccc ttc gcc aac cga ccc atc aat gag cag aaa cgt ttc cga 245
 Leu Ala Pro Phe Ala Asn Arg Pro Ile Asn Glu Gln Lys Arg Phe Arg
 60 65 70 75

cct gcc gtg aag agc cga tca cga cga gcg ccg ccg tgc gta tgg aag 293
 Pro Ala Val Lys Ser Arg Ser Arg Arg Ala Pro Pro Cys Val Trp Lys
 80 85 90

gtg tgt ccc gct ccc ccc tgg ctg gtc acc aaa cgt aaa cag gaa acc 341
 Val Cys Pro Ala Pro Pro Trp Leu Val Thr Lys Arg Lys Gln Glu Thr
 95 100 105

agc gac tac tgacgtcata cctcaataga ccgactcatg acttcaacgc 390
 Ser Asp Tyr
 110

tgaattgacc tcaccgagag ctccaacgtc acagcaggag cgagagagag agagagagag 450
 agagagagag aaaggctgga gtatttctct ttctttcggg ttttcgtggt gaagtgtgat 510
 cagctgggct ggttcaaaat tggtgaataa agttgaataa aaaaaaaaaa aaaaaaagta 570
 ctctgcgttg ttactcgagc ttaagggcga attc 604

<210> 173
 <211> 110
 <212> PRT
 <213> Conus nobilis

<400> 173
 Met Gln Thr Ala Tyr Trp Val Met Met Met Val Val Val Met Met Val
 1 5 10 15
 Gly Val Thr Val Ala Gly Ser Leu Ser Val Phe Asp Asp Asp Asn Asp
 20 25 30
 Ser Asp Pro Ala Val Lys Arg Ala Ile Thr Trp Ser Arg Phe Leu Gly
 35 40 45
 Ala Ser Pro Ala Phe Leu Ala Gln Gln Arg Ala Leu Ala Pro Phe Ala
 50 55 60
 Asn Arg Pro Ile Asn Glu Gln Lys Arg Phe Arg Pro Ala Val Lys Ser
 65 70 75 80
 Arg Ser Arg Arg Ala Pro Pro Cys Val Trp Lys Val Cys Pro Ala Pro
 85 90 95
 Pro Trp Leu Val Thr Lys Arg Lys Gln Glu Thr Ser Asp Tyr
 100 105 110

<210> 174
 <211> 37
 <212> PRT
 <213> Conus nobilis

<220>
 <221> PEPTIDE
 <222> (1)..(37)
 <223> Xaa at residues 3, 13, 14, 21, 23 and 24 may be Pro or hydroxy-Pr
 o; Xaa at residues 17 and 25 may be Trp (D or L) or bromo-Trp (D
 or L); Xaa at residue 33 may be Glu or Gla;

<220>
 <221> PEPTIDE
 <222> (1)..(37)
 <223> Xaa at residue 37 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty
 r, O-sulpho-Tyr or O-phospho-Tyr

<400> 174
 Phe Arg Xaa Ala Val Lys Ser Arg Ser Arg Arg Ala Xaa Xaa Cys Val
 1 5 10 15
 Xaa Lys Val Cys Xaa Ala Xaa Xaa Xaa Leu Val Thr Lys Arg Lys Gln
 20 25 30

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<400>      176
Met  Gln  Thr  Ala  Tyr  Trp  Val  Met  Val  Met  Met  Met  Val  Val  Trp  Ile
1              5              10              15

Thr  Ala  Pro  Leu  Ser  Glu  Gly  Gly  Lys  Pro  Lys  His  Ala  Ile  Arg  Gly
                20              25              30

Leu  Val  Pro  Asp  Asp  Leu  Thr  Pro  Gln  Leu  Ile  Leu  Arg  Ser  Leu  Ile
                35              40              45

Ser  Arg  Arg  Ser  Ser  Phe  Gly  Lys  Asp  Ala  Lys  Pro  Pro  Phe  Ser  Cys
        50              55              60

Ser  Gly  Leu  Arg  Gly  Gly  Cys  Val  Leu  Pro  Pro  Asn  Leu  Arg  Pro  Lys
65              70              75              80

Phe  Asn  Lys  Gly  Gly

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85

<210> 177
 <211> 25
 <212> PRT
 <213> Conus parius

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residues 1, 3, 15, 16 and 20 may be Pro or hydroxy-Pro

<400> 177
 Xaa Xaa Phe Ser Cys Ser Gly Leu Arg Gly Gly Cys Val Leu Xaa Xaa
 1 5 10 15
 Asn Leu Arg Xaa Lys Phe Asn Lys Gly
 20 25

<210> 178
 <211> 390
 <212> DNA
 <213> Conus parius

<220>
 <221> CDS
 <222> (19)..(273)

<400> 178
 gaattcgccc ttggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 51
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met
 1 5 10
 atg gtg atg tgg att aca gcc cct ctg tct gaa ggt ggt aaa ccg aag 99
 Met Val Met Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Pro Lys
 15 20 25
 ctc ata att cgg ggt ttg gtg cca aac gac tta acc cca cag cgt atc 147
 Leu Ile Ile Arg Gly Leu Val Pro Asn Asp Leu Thr Pro Gln Arg Ile
 30 35 40
 ttg cga agt ctg att tcc ggg cgt act tat ggc atc tat gat gcg aaa 195
 Leu Arg Ser Leu Ile Ser Gly Arg Thr Tyr Gly Ile Tyr Asp Ala Lys
 45 50 55
 ccc ccc ttt agt tgt gca ggc ctc cga ggg ggt tgc gtc cta cct ccc 243
 Pro Pro Phe Ser Cys Ala Gly Leu Arg Gly Gly Cys Val Leu Pro Pro
 60 65 70 75
 aat ctc agg cca aag ttc aag gaa ggt cga taaaaaaccc aagcgttcct 293
 Asn Leu Arg Pro Lys Phe Lys Glu Gly Arg
 80 85
 agttatacga atgccagcaa ataaaagcag tttgattgcg aaaaaaaaaa aaaaaaaaaa 353
 gtactctgcg ttgttactcg agcttaaggg cgaattc 390

<210> 179
 <211> 85
 <212> PRT
 <213> Conus parius

<400> 179
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Met Trp Ile

gct gac cta tgt atc cac aag att tgt cca cca cgg tat cac caa agc 245
Ala Asp Leu Cys Ile His Lys Ile Cys Pro Pro Arg Tyr His Gln Ser
60 65 70 75

caa caa taaaagacgt cagacaacca ccacaacttt agtatgacat cgttaatagg 301
Gln Gln

acttcagcaa gtattttaac atcactgtgg ttgtgatgaa atcagtcgcc ttaaaagatt 361

ggctttttcc ttgtttaaga gttgtacttg tatkagcttt gcacttcgaa ataaagttga 421
tgtgatgaac caaaaaaaaa aaaaaaaaaa agtactctgc gttgttactc gagcttaagg 481

gcgaattc 489

<210> 182

<211> 77

<212> PRT

<213> Conus planorbis

<400> 182

Met Gln Thr Ala Tyr Trp Val Met Met Met Met Met Val Trp Ile Thr
1 5 10 15

Gly His Leu Ser Glu Gly Gly Lys Leu Lys Asp Ala Ile Arg Gly Leu
20 25 30

Val Pro Asp Asp Leu Thr Ser Met Phe Ala Leu His Leu Pro Val Ser
35 40 45

His Ser Arg Ser Ser Ser Asn Gly Leu Lys Arg Ala Asp Leu Cys Ile
50 55 60

His Lys Ile Cys Pro Pro Arg Tyr His Gln Ser Gln Gln
65 70 75

<210> 183

<211> 26

<212> PRT

<213> Conus planorbis

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residues 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue 21 may be Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 183

Ser Ser Ser Asn Gly Leu Lys Arg Ala Asp Leu Cys Ile His Lys Ile
1 5 10 15

Cys Xaa Xaa Arg Xaa His Gln Ser Gln Gln
20 25

<210> 184

<211> 834

<212> DNA

<213> Conus pulicarius

<220>

<221> CDS

<222> (1)..(246)

<220>

<221> misc_feature

<222> (1)..(834)

<223> n may be any nucleotide

<400> 184
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg atg gtg tgg gtt 48
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Met Val Trp Val
 1 5 10 15

aca gcg cct gtg tct gaa ggt ggt aaa ttg agc gac gta att cgg ggt 96
 Thr Ala Pro Val Ser Glu Gly Gly Lys Leu Ser Asp Val Ile Arg Gly
 20 25 30

ttg gtg cca gac gac ata acc cca cag att att ttg caa agt ctg aat 144
 Leu Val Pro Asp Asp Ile Thr Pro Gln Ile Ile Leu Gln Ser Leu Asn
 35 40 45

gcc agt cgt cat gct tac aga cgt gtt cgt ctg aga gga cag ata tgt 192
 Ala Ser Arg His Ala Tyr Arg Arg Val Arg Leu Arg Gly Gln Ile Cys
 50 55 60

atc tgg aag gta tgt cca cca cta cta caa tgg ata cat cca tta gta 240
 Ile Trp Lys Val Cys Pro Pro Leu Leu Gln Trp Ile His Pro Leu Val
 65 70 75 80

aaa aga tgaatgacat cagacaaccg ccacaactgt agtacgacat cgттаacacg 296
 Lys Arg

acttcagcaa atattctaac atcacagtgg gttgtgaaga natcggggttg gctttaaaaa 356

aaanaatggg ggnttttccc cntgggttta aaaaaanntn ggnnccgggn aannncccn 416

nnnnnncccc ccccnntngg gagaaaaaaa aaannccnnt nnnnggggggn nnnncaaaaa 476

aaaaaaaaa aaaaaaaaaa aaaaancccc nggggggngtg ntttnncccc cncccccngg 536

ggggggggggn gnttttncccc ccccccgng gggggggggg nttttntttt nngggggngc 596

cccccccccc cccnnncnnn nnaanaannn nngggggggg ggaanaaaaa nannnnnnnn 656

nnnnnnnnnn tttntcnnt cncnccngnn gnnaaaaaaa aaanttnatt tntnnannnc 716

nnnnnnccnn cnnnnaacc nccccnnc ncnnncannn nagannanga ggggggggng 776

nnnnngngna nnnnnannnn nnngaannng agngngnnn cncnncnncg cncnngnc 834

<210> 185
 <211> 82
 <212> PRT
 <213> Conus pulicarius

<400> 185
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Met Val Trp Val
 1 5 10 15

Thr Ala Pro Val Ser Glu Gly Gly Lys Leu Ser Asp Val Ile Arg Gly
 20 25 30

Leu Val Pro Asp Asp Ile Thr Pro Gln Ile Ile Leu Gln Ser Leu Asn
 35 40 45

Ala Ser Arg His Ala Tyr Arg Arg Val Arg Leu Arg Gly Gln Ile Cys
 50 55 60

Ile Trp Lys Val Cys Pro Pro Leu Leu Gln Trp Ile His Pro Leu Val
 65 70 75 80

<210>	188
<211>	82
<212>	PRT

<213> Conus pulicarius

<400> 188

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Met Val Trp Val
1 5 10 15

Thr Ala Pro Val Ser Glu Gly Gly Lys Leu Ser Asp Val Ile Arg Gly
20 25 30

Leu Val Pro Asp Asp Leu Thr Pro Gln Ile Ile Leu Gln Ser Leu Asn
35 40 45

Ala Ser Arg His Ala Tyr Arg Arg Val Arg Pro Arg Gly Gln Ile Cys
50 55 60

Ile Trp Lys Val Cys Pro Pro Leu Leu Gln Trp Ile His Pro Leu Val
65 70 75 80

Lys Arg

<210> 189

<211> 26

<212> PRT

<213> Conus pulicarius

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residues 3, 14, 15 and 22 may be Pro or hydroxy-Pro; Xaa at residues 10 and 19 may be Trp (D or L) or bromo-Trp (D or L)

<400> 189

Val Arg Xaa Arg Gly Gln Ile Cys Ile Xaa Lys Val Cys Xaa Xaa Leu
1 5 10 15

Leu Gln Xaa Ile His Xaa Leu Val Lys Arg
20 25

<210> 190

<211> 471

<212> DNA

<213> Conus pulicarius

<220>

<221> CDS

<222> (1)..(246)

<400> 190

atg cag acg gcc tac tgg gtg atg gtg atg atg atg atg gtg tgg gtt 48
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Met Val Trp Val
1 5 10 15

aca gcg cct gtg tct gaa ggt ggt aaa ttg agc gac gta att cgg ggt 96
Thr Ala Pro Val Ser Glu Gly Gly Lys Leu Ser Asp Val Ile Arg Gly
20 25 30

ttg gtg cca gac gac ata acc cca cag att atc ttg caa agt ctg aat 144
Leu Val Pro Asp Asp Ile Thr Pro Gln Ile Ile Leu Gln Ser Leu Asn
35 40 45

gcc agt cgt cat gct tac aga cct gtt cgt ctg aga gga cag ata tgt 192
Ala Ser Arg His Ala Tyr Arg Pro Val Arg Leu Arg Gly Gln Ile Cys
50 55 60

atc tgg aag gta tgt cca cca cta cta caa tgg ata cat cca tta gta 240

Ile Trp Lys Val Cys Pro Pro Leu Leu Gln Trp Ile His Pro Leu Val
65 70 75 80

aaa aga tgaatgacat cagacaaccg ccacaactgt agtacgacat cgттаacacg 296
Lys Arg

acttcagcaa atattttaac atcacagtgg ttgtgaagaa atcggttgct ttaaaaaaag 356

attgggtttt tccttgttta agagttgtac tgatatcagt tctgcactat gaaataaagc 416

tgatgtgacg aacaaaaaaa aaaaaaaaaa aaagtactct gcgttgttac tcgag 471

<210> 191

<211> 82

<212> PRT

<213> Conus pulicarius

<400> 191

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Met Val Trp Val
1 5 10 15

Thr Ala Pro Val Ser Glu Gly Gly Lys Leu Ser Asp Val Ile Arg Gly
20 25 30

Leu Val Pro Asp Asp Ile Thr Pro Gln Ile Ile Leu Gln Ser Leu Asn
35 40 45

Ala Ser Arg His Ala Tyr Arg Pro Val Arg Leu Arg Gly Gln Ile Cys
50 55 60

Ile Trp Lys Val Cys Pro Pro Leu Leu Gln Trp Ile His Pro Leu Val
65 70 75 80

Lys Arg

<210> 192

<211> 27

<212> PRT

<213> Conus pulicarius

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residues 1, 15, 16 and 23 may be Pro or hydroxy-Pro; Xaa at residues 11 and 20 may be Trp (D or L) or bromo-Trp (D or L)

<400> 192

Xaa Val Arg Leu Arg Gly Gln Ile Cys Ile Xaa Lys Val Cys Xaa Xaa
1 5 10 15

Leu Leu Gln Xaa Ile His Xaa Leu Val Lys Arg
20 25

<210> 193

<211> 375

<212> DNA

<213> Conus rattus

<220>

<221> CDS

<222> (1)..(282)

<400> 193

atg cag acg gcc tac tgg gtg atg gtg atg atg gtg gtg gtg ggg ttc 48
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Val Val Val Gly Phe
1 5 10 15

acc gtc ggg ggt cac gtc cat caa tct cac agt cct aca tcg cgc agc 96
Thr Val Gly Gly His Val His Gln Ser His Ser Pro Thr Ser Arg Ser
20 25 30

cat ggt gat gac tcc att cat gac aag acg att cat caa cat ctg ttt 144
His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His Leu Phe
35 40 45

gcc cgt ctt cct ctg gag aac aac gac gac cat cgt tct gtg gat ctt 192
Ala Arg Leu Pro Leu Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu
50 55 60

cct gca ggg acc agc gca ggc gac atg aaa cca caa cgc caa aga cgt 240
Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln Arg Arg
65 70 75 80

ctc tgc tgc atc ttt gcc att ctt tgg ttc tgt tgt ctc ggt 282
Leu Cys Cys Ile Phe Ala Ile Leu Trp Phe Cys Cys Leu Gly
85 90

taacagtaca aattgcaatg cactggccga ttgaaagaac tgcaataaac ggaaaaaaaa 342

aaaaaaaaaa agtactctgc gttgttactc gag 375

<210> 194
<211> 94
<212> PRT
<213> Conus rattus

<400> 194
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Val Val Val Gly Phe
1 5 10 15

Thr Val Gly Gly His Val His Gln Ser His Ser Pro Thr Ser Arg Ser
20 25 30

His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His Leu Phe
35 40 45

Ala Arg Leu Pro Leu Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu
50 55 60

Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln Arg Arg
65 70 75 80

Leu Cys Cys Ile Phe Ala Ile Leu Trp Phe Cys Cys Leu Gly
85 90

<210> 195
<211> 13
<212> PRT
<213> Conus rattus

<220>
<221> PEPTIDE
<222> (1)..(13)
<223> Xaa at residue 9 may be Trp (D or L) or bromo-Trp (D or L)

<400> 195
Leu Cys Cys Ile Phe Ala Ile Leu Xaa Phe Cys Cys Leu

1 5 10

<210> 196
 <211> 494
 <212> DNA
 <213> Conus striatus

<220>
 <221> CDS
 <222> (21)..(287)

<400> 196
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met
 1 5 10

atg gtg tgg att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac 101
 Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp
 15 20 25

gta att cgg ggt ttg gtg cca cac atc tta acc cca cag cat atc ttg 149
 Val Ile Arg Gly Leu Val Pro His Ile Leu Thr Pro Gln His Ile Leu
 30 35 40

caa agt ctg att tcc cct ctt cgt tct aac aac ggt cgt tcg agt gga 197
 Gln Ser Leu Ile Ser Pro Leu Arg Ser Asn Asn Gly Arg Ser Ser Gly
 45 50 55

gca caa ata tgc atc tgg aag gta tgt cca cca tcc cca tgg aga caa 245
 Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Gln
 60 65 70 75

cca caa gaa atg atg aat gac atc aga caa ccg cca caa ctg 287
 Pro Gln Glu Met Met Asn Asp Ile Arg Gln Pro Pro Gln Leu
 80 85

tagtacgaca tcgttgatac gacttttagca aatatttttaa catcactgtg gttgtgaaga 347

aatcagttgc tttaaaagat tggatttttc cttgtttaag agttgtactg atatcagctc 407

tgcactatga aataaagctg atgtgacaaa caaaaaaaaaa aaaaaaaaaa gtactctgcg 467

ttgttactcg agcttaaggg cgaattc 494

<210> 197
 <211> 89
 <212> PRT
 <213> Conus striatus

<400> 197
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
 1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30

Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Ile Ser
 35 40 45

Pro Leu Arg Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile
 50 55 60

Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Gln Pro Gln Glu Met Met
 65 70 75 80

Asn Asp Ile Arg Gln Pro Pro Gln Leu
85

<210> 198
<211> 38
<212> PRT
<213> Conus striatus

<220>
<221> PEPTIDE
<222> (1)..(38)
<223> Xaa at residues 14 and 22 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 18, 19, 21, 25, 35 and 36 may be Pro or hydroxy-Pro; Xaa at residue 27 may be Glu or Gla

<400> 198
Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile Xaa Lys Val
1 5 10 15

Cys Xaa Xaa Ser Xaa Xaa Arg Gln Xaa Gln Xaa Met Met Asn Asp Ile
20 25 30

Arg Gln Xaa Xaa Gln Leu
35

<210> 199
<211> 412
<212> DNA
<213> Conus striolatus

<220>
<221> CDS
<222> (1)..(240)

<400> 199
atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
1 5 10 15

gac cct ctg tct gaa ggt ggt aaa ttg aac gac gta att cgg ggt ttg 96
Asp Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
20 25 30

gtg cca cgc atc tta acc cca cag cat acc ttg cga agt ccg act tcc 144
Val Pro Arg Ile Leu Thr Pro Gln His Thr Leu Arg Ser Pro Thr Ser
35 40 45

ctt ctt cgt tct aac acc ggt ggt tcg agt gga gca caa ata tgc atc 192
Leu Leu Arg Ser Asn Thr Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile
50 55 60

tgg aag gta tgt cca cca tcc cca tgg aga cga tca caa gga aaa aga 240
Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Ser Gln Gly Lys Arg
65 70 75 80

tgaatgacgt cagacaagcg ccacaactgt agtacgacat cgttgatagc acttcagcaa 300

gtatttttaac atcaactgtgg ttgtgaagaa atcagttgct ttaaaagatt ggattttttcc 360

ttgttttaaga gttgtactga tatcagctct gccctgtgaa ataaagctga tg 412

<210> 200
<211> 80
<212> PRT

<213> Conus striolatus

<400> 200

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
1 5 10 15

Asp Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
20 25 30

Val Pro Arg Ile Leu Thr Pro Gln His Thr Leu Arg Ser Pro Thr Ser
35 40 45

Leu Leu Arg Ser Asn Thr Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile
50 55 60

Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Ser Gln Gly Lys Arg
65 70 75 80

<210> 201

<211> 26

<212> PRT

<213> Conus striolatus

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residues 14 and 22 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 18, 19 and 21 may be Pro or hydroxy-Pro

<400> 201

Ser Asn Thr Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Xaa Lys Val
1 5 10 15

Cys Xaa Xaa Ser Xaa Xaa Arg Arg Ser Gln
20 25

<210> 202

<211> 412

<212> DNA

<213> Conus striolatus

<220>

<221> CDS

<222> (1)..(240)

<400> 202

atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
1 5 10 15

gcc cct ctg tct gaa ggt ggt aaa ttg aac gac gta att cgg ggt ttg 96
Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
20 25 30

gtg cca cac atc tta acc cca cag cat atc ttg caa agt ctg att tcc 144
Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Ile Ser
35 40 45

cct ctt cgt tct aac aac ggt cgt tcg agt gga gca caa ata tgc atc 192
Pro Leu Arg Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile
50 55 60

tgg aag gta tgt cca cca tcc cca tgg aga cga tca caa gga aaa aga 240
Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Ser Gln Gly Lys Arg
65 70 75 80

tgaatgacgt cagacaagcg ccacaactgt agtacgacat cgttgatacg acttcagcaa 300
 gtattttaac atcactgtgg ttgtgaagaa atcagttgct ttaaaagatt ggatttttcc 360
 ttgtttaaga gttgtactga tatcagctct gcaactgtgaa ataaagctga tg 412

<210> 203
 <211> 80
 <212> PRT
 <213> Conus striolatus

<400> 203
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
 1 5 10 15
 Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30
 Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Ile Ser
 35 40 45
 Pro Leu Arg Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile
 50 55 60
 Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Ser Gln Gly Lys Arg
 65 70 75 80

<210> 204
 <211> 26
 <212> PRT
 <213> Conus striolatus
 <220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residues 14 and 22 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 18, 19 and 21 may be Pro or hydroxy-Pro

<400> 204
 Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile Xaa Lys Val
 1 5 10 15
 Cys Xaa Xaa Ser Xaa Xaa Arg Arg Ser Gln
 20 25

<210> 205
 <211> 497
 <212> DNA
 <213> Conus striolatus

<220>
 <221> CDS
 <222> (21)..(257)

<400> 205
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met
 1 5 10
 atg gtg tgg att aaa gac cct ctg tct gaa ggt ggt aaa ttg aac gac 101
 Met Val Trp Ile Lys Asp Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp
 15 20 25

gta att cgg ggt ttg gtg cca cac atc tta acc cca cag cat atc ttg 149
Val Ile Arg Gly Leu Val Pro His Ile Leu Thr Pro Gln His Ile Leu
30 35 40

caa agt ctg att tcc cct ctt cgt tct aac aac ggt cgt tcg agt gga 197
Gln Ser Leu Ile Ser Pro Leu Arg Ser Asn Asn Gly Arg Ser Ser Gly
45 50 55

gca caa ata tgc aac tgg aag gta tgt cca cca tcc cca tgg aga cga 245
Ala Gln Ile Cys Asn Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Arg
60 65 70 75

cca cga gga aaa tgatgaatga catcagacaa ccgccacaac tgtagtacga 297
Pro Arg Gly Lys

cttcgttgat acgacttttag caaatatttt aacatcactg tggttgtgaa gaaatcagtt 357

gctttaaaaag attggatttt tccttgttta agagttgtac tgatatcagc tctgcactat 417

gaaataaagc tgatgtgaca aacaaaaaaaa aaaaaaaaaa aaagtactct gcgttgttac 477

tcgagcttaa gggcgaattc 497

<210> 206

<211> 79

<212> PRT

<213> Conus striolatus

<400> 206

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Lys
1 5 10 15

Asp Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
20 25 30

Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Ile Ser
35 40 45

Pro Leu Arg Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Asn
50 55 60

Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Pro Arg Gly Lys
65 70 75

<210> 207

<211> 26

<212> PRT

<213> Conus striolatus

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residues 14 and 22 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 18, 19, 21 and 25 may be Pro or hydroxy-Pro

<400> 207

Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Asn Xaa Lys Val
1 5 10 15

Cys Xaa Xaa Ser Xaa Xaa Arg Arg Xaa Arg
20 25

<210> 208

<211> 496

<212> DNA
 <213> Conus striolatus

<220>
 <221> CDS
 <222> (21)..(287)

<400> 208
 gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met
 1 5 10

atg gtg tgg att aca gcc cct ctg tct gaa ggt ggt aaa ttg aac gac 101
 Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp
 15 20 25

gta att cgg ggt ttg gtg cca cac atc tta acc cca cag cat atc ttg 149
 Val Ile Arg Gly Leu Val Pro His Ile Leu Thr Pro Gln His Ile Leu
 30 35 40

caa agt ctg att tcc cct ctt cgt tct aac aac ggt cgt tcg agt gga 197
 Gln Ser Leu Ile Ser Pro Leu Arg Ser Asn Asn Gly Arg Ser Ser Gly
 45 50 55

gca caa ata tgc atc tgg aag gta tgt cca cca tcc cca tgg aga caa 245
 Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Gln
 60 65 70 75

cca caa gaa atg atg aat gac atc aga caa ccg cca caa ctg 287
 Pro Gln Glu Met Met Asn Asp Ile Arg Gln Pro Pro Gln Leu
 80 85

tagtacgaca tcgttgatcac gacttttagca aatatttttaa catcactgtg gttgtgaaga 347

aatcagttgc tttaaaagat tggatttttc cttgtttaag agttgtactg atatcagctc 407
 tgcactatga aataaagctg atgtgacaaa cgaaaaaaaaa aaaaaaaaaa aagtactctg 467

cgttgttact cgagcttaag ggcgaattc 496

<210> 209
 <211> 89
 <212> PRT
 <213> Conus striolatus

<400> 209
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
 1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30

Val Pro His Ile Leu Thr Pro Gln His Ile Leu Gln Ser Leu Ile Ser
 35 40 45

Pro Leu Arg Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile
 50 55 60

Trp Lys Val Cys Pro Pro Ser Pro Trp Arg Gln Pro Gln Glu Met Met
 65 70 75 80

Asn Asp Ile Arg Gln Pro Pro Gln Leu
 85

<210> 210

<211> 38
 <212> PRT
 <213> Conus striolatus

<220>
 <221> PEPTIDE
 <222> (1)..(38)
 <223> Xaa at residues 14 and 22 may be Trp (D or L) or bromo-Trp (D or L); Xaa at residues 18, 19, 21, 25, 35 and 36 may be Pro or hydroxy-Pro; Xaa at residue 27 may be Glu or Gla

<400> 210
 Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile Xaa Lys Val
 1 5 10 15

Cys Xaa Xaa Ser Xaa Xaa Arg Gln Xaa Gln Xaa Met Met Asn Asp Ile
 20 25 30

Arg Gln Xaa Xaa Gln Leu
 35

<210> 211
 <211> 413
 <212> DNA
 <213> Conus sulcatus

<220>
 <221> CDS
 <222> (1)..(234)

<400> 211
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
 1 5 10 15

gcc tct ctg tct gaa ggt ggt aaa ccg aac gac gtc att cgg ggt ttt 96
 Ala Ser Leu Ser Glu Gly Gly Lys Pro Asn Asp Val Ile Arg Gly Phe
 20 25 30

gtg cca gac gac tta acc cca cag ctt atc ttg cga agt ctg att tcc 144
 Val Pro Asp Asp Leu Thr Pro Gln Leu Ile Leu Arg Ser Leu Ile Ser
 35 40 45

cgt cgt cgt tct gac aag gat gtt ggg aag aga atg gaa tgt tac tgg 192
 Arg Arg Arg Ser Asp Lys Asp Val Gly Lys Arg Met Glu Cys Tyr Trp
 50 55 60

aag gca tgt aga ccc acg cta tcg aga cga cat gat ctt ggg 234
 Lys Ala Cys Arg Pro Thr Leu Ser Arg Arg His Asp Leu Gly
 65 70 75

taaaagatga atgacgtcag acaacagcca caactatagt atgacatcgt taatacgact 294

tcagcaaata ttttaacatc actgtggttg tgaagaaatc agttgcttta aaagattgga 354

tttttccgtg tttaagagtt gtactgatat cagctctgcc ctgtgaaata aagctgatg 413

<210> 212
 <211> 78
 <212> PRT
 <213> Conus sulcatus

<400> 212
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr

[illegible]

taagaaaaga aacaattgac gtcagacaac cgccacaact tgagtaacgac atcgtaata 294
 caacttcagc aaatatgaaa ttttcagcat cactgtggtt gtgaagaaat cagttgcttt 354
 aaaagattgg atttgcctt gtttaagagt tgtactgatg tcatctctgc actgtgaaat 414
 aaagctgatg tgacaaacaa aaaaaaaaaa aaaaaagtac tctgcgttgt tactcgag 472

<210> 215
 <211> 78
 <212> PRT
 <213> Conus terebra

<400> 215
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
 1 5 10 15

Ala Pro Leu Ser Glu Gly Asp Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30

Val Pro Asp Asn Leu Ala Pro Gln Leu Val Leu Gln Ser Leu Asp Ser
 35 40 45

Arg Arg His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile
 50 55 60

Trp Lys Ile Cys Pro Pro Ser Pro Trp Lys Arg Leu Gly Ser
 65 70 75

<210> 216
 <211> 28
 <212> PRT
 <213> Conus terebra

<220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> Xaa at residues 2, 19, 20 and 22 may be Pro or hydroxy-Pro; Xaa at
 residues 15 and 23 may be Trp (D or L) or bromo-Trp (D or L)

<400> 216
 His Xaa His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile Xaa Lys
 1 5 10 15

Ile Cys Xaa Xaa Ser Xaa Xaa Lys Arg Leu Gly Ser
 20 25

<210> 217
 <211> 474
 <212> DNA
 <213> Conus terebra

<220>
 <221> CDS
 <222> (1)..(234)

<400> 217
 atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg tgg att aca 48
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
 1 5 10 15

gcc cct ctg tct gaa ggt gat aaa ttg aac gac gta att cgg ggt ttg 96
 Ala Pro Leu Ser Glu Gly Asp Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30

gtg cca gat aac tta gcc cca cag ctt gtt ttg cat agt ctg gat tcc 144
 Val Pro Asp Asn Leu Ala Pro Gln Leu Val Leu His Ser Leu Asp Ser
 35 40 45

cgt cgt cat cct cac ggc att cgt cag gat gga gcc caa ata tgt atc 192
 Arg Arg His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile
 50 55 60

tgg aag ata tgt cca cca tcc cca tgg aga cga ctt gga tct 234
 Trp Lys Ile Cys Pro Pro Ser Pro Trp Arg Arg Leu Gly Ser
 65 70 75

taagaaaaga aacaattgac gtcagacaac cgccacatct tgagtacgac atcgттаата 294

cgacttcagc aaatatgaaa ttttcagcat cactgtgggt gtgaagaaat cagttgcctt 354

aaaagattgg atttgtcctt gtttaagagt tgtactgatg tcactctctgc actatgaaat 414

aaagctgatg tgacaaacaa aaaaaaaaaa aaaaaaaagt actctgcggt gttactcgag 474

<210> 218

<211> 78

<212> PRT

<213> Conus terebra

<400> 218

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
 1 5 10 15

Ala Pro Leu Ser Glu Gly Asp Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30

Val Pro Asp Asn Leu Ala Pro Gln Leu Val Leu His Ser Leu Asp Ser
 35 40 45

Arg Arg His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile
 50 55 60

Trp Lys Ile Cys Pro Pro Ser Pro Trp Arg Arg Leu Gly Ser
 65 70 75

<210> 219

<211> 28

<212> PRT

<213> Conus terebra

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residues 2, 19, 20 and 22 may be Pro or hydroxy-Pro; Xaa a
 t residues 15 and 23 may be Trp (D or L) or bromo-Trp (D or L)

<400> 219

His Xaa His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile Xaa Lys
 1 5 10 15

Ile Cys Xaa Xaa Ser Xaa Xaa Arg Arg Leu Gly Ser
 20 25

<210> 220

<211> 485

<212> DNA

<213> Conus vexillum

<220>
 <221> CDS
 <222> (21)..(236)

<400> 220
 gaattcgccc ttatggatcc atg cag atg gcc tac tgg gtg atg gtg atg atg 53
 Met Gln Met Ala Tyr Trp Val Met Val Met Met
 1 5 10

atg gtg tgg att aaa ggc cct gtg tcc gaa ggt ggt aaa ttg aac gac 101
 Met Val Trp Ile Lys Gly Pro Val Ser Glu Gly Gly Lys Leu Asn Asp
 15 20 25

gta att cgg ggt ttg gtg cca gac gac ttg acc cca gtg tct gcc ttg 149
 Val Ile Arg Gly Leu Val Pro Asp Asp Leu Thr Pro Val Ser Ala Leu
 30 35 40

cat cat ccg gtt tcc cat cgt cgg tct cac agc agt agt ttg tgg tgt 197
 His His Pro Val Ser His Arg Arg Ser His Ser Ser Ser Leu Trp Cys
 45 50 55

gta tgt cca ttc agg gtg tgt cca cca tgc cat gga aga tgacctggtc 246
 Val Cys Pro Phe Arg Val Cys Pro Pro Cys His Gly Arg
 60 65 70

ccaaaccaac aaaataacgt cagacaaccg ccacaacttt agtacgacat cccttaatac 306
 gacttcagca agtatttttaa catcactatg gtgtgatgaa atcagttgct ttaaaagatt 366
 ggattttttcc ttgtttaaga gttgcactga taacagccca gcagtatgaa ataaagttga 426
 tgtggcaaaa aaaaaaaaaa aagtactctg cgttgttact cgagcttaag ggcgaattc 485

<210> 221
 <211> 72
 <212> PRT
 <213> Conus vexillum

<400> 221
 Met Gln Met Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Lys
 1 5 10 15

Gly Pro Val Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Leu
 20 25 30

Val Pro Asp Asp Leu Thr Pro Val Ser Ala Leu His His Pro Val Ser
 35 40 45

His Arg Arg Ser His Ser Ser Ser Leu Trp Cys Val Cys Pro Phe Arg
 50 55 60

Val Cys Pro Pro Cys His Gly Arg
 65 70

<210> 222
 <211> 19
 <212> PRT
 <213> Conus vexillum

<220>
 <221> PEPTIDE
 <222> (1)..(19)
 <223> Xaa at residue 7 may be Trp (D or L) or bromo-Trp (D or L); Xaa a

t residues 11, 16 and 17 may be Pro or hydroxy-Pro

<400> 222

Ser His Ser Ser Ser Leu Xaa Cys Val Cys Xaa Phe Arg Val Cys Xaa
1 5 10 15

Xaa Cys His

<210> 223

<211> 481

<212> DNA

<213> Conus vexillum

<220>

<221> CDS

<222> (21)..(257)

<400> 223

gaattcgccc ttatggatcc atg cag acg gcc tac tgg gtg atg gtg atg atg 53
Met Gln Thr Ala Tyr Trp Val Met Val Met Met
1 5 10

atg gtg tgg att aca gcc cct ttg tct gaa ggt ggt aaa ctg aac gat 101
Met Val Trp Ile Thr Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp
15 20 25

gta att cgg ggt ttc gcg cta gat gac tta gcc caa agc cgt att atg 149
Val Ile Arg Gly Phe Ala Leu Asp Asp Leu Ala Gln Ser Arg Ile Met
30 35 40

caa agt ctg gtt ttc agt cat cag cct ctt cca acg gca tcc ata tgt 197
Gln Ser Leu Val Phe Ser His Gln Pro Leu Pro Thr Ala Ser Ile Cys
45 50 55

atc tgg aag ata tgt cca cca gac cca tgg aga cga cat gat ctt cag 245
Ile Trp Lys Ile Cys Pro Pro Asp Pro Trp Arg Arg His Asp Leu Gln
60 65 70 75

aaa agt aac aaa tgacgtcaga caaccgccac aacttgaata caacatcatt 297
Lys Ser Asn Lys

aatacgactt cagcaaatat tttagcatca ctgtgattgt tcggaagtca gttgctttaa 357

aagattggat ttgtccctgt tgtattgatg tcaactctgc actatgaaat aaagctgatg 417

tgacaagcaa aaaaaaaaaa aaaaaaagta ctctgcgttg ttactcgagc ttaagggcga 477

attc 481

<210> 224

<211> 79

<212> PRT

<213> Conus vexillum

<400> 224

Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Trp Ile Thr
1 5 10 15

Ala Pro Leu Ser Glu Gly Gly Lys Leu Asn Asp Val Ile Arg Gly Phe
20 25 30

Ala Leu Asp Asp Leu Ala Gln Ser Arg Ile Met Gln Ser Leu Val Phe
35 40 45

Ser His Gln Pro Leu Pro Thr Ala Ser Ile Cys Ile Trp Lys Ile Cys
50 55 60

Pro Pro Asp Pro Trp Arg Arg His Asp Leu Gln Lys Ser Asn Lys
65 70 75

<210> 225
<211> 38
<212> PRT
<213> Conus vexillum

<220>
<221> PEPTIDE
<222> (1)..(38)
<223> Xaa at residues 11, 14, 24, 25 and 27 may be Pro or hydroxy-Pro;
Xaa at residues 20 and 28 may be Trp (D or L) or bromo-Trp (D or L)

<400> 225
Ile Met Gln Ser Leu Val Phe Ser His Gln Xaa Leu Xaa Thr Ala Ser
1 5 10 15

Ile Cys Ile Xaa Lys Ile Cys Xaa Xaa Asp Xaa Xaa Arg Arg His Asp
20 25 30

Leu Gln Lys Ser Asn Lys
35

<210> 226
<211> 384
<212> DNA
<213> Conus vexillum

<220>
<221> CDS
<222> (1)..(285)

<400> 226
atg cag acg gcc tac tgg gtg atg gtg atg atg atg gtg gtg ggg ttc 48
Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Gly Phe
1 5 10 15

acc gtc gag agt cac gtc cat cag tct cac agt cct aca tcg cgc agc 96
Thr Val Glu Ser His Val His Gln Ser His Ser Pro Thr Ser Arg Ser
20 25 30

cat ggt gat gac tcc att cat gac aag acg att cat caa cat ctg ttt 144
His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His Leu Phe
35 40 45

gcc cgt ctt cct ctg gag aac aac gac gac cat cgt tct gtg gat ctt 192
Ala Arg Leu Pro Leu Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu
50 55 60

cct gca ggg act agc gca ggc gac atg aaa cca caa cgc cag aaa cgt 240
Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln Lys Arg
65 70 75 80

ttc tgc tgc atc ttt gcc ccg att ctt ttg ttc tgt tgt ttc ggt 285
Phe Cys Cys Ile Phe Ala Pro Ile Leu Leu Phe Cys Cys Phe Gly
85 90 95

taacagcaca aattacactg cactggccga ttgaaagaac tgcaataaac ggtaaagcaa 345

aaaaaaaaaa aaaaaaagta ctctgcgttg ttactcgag

384

<210> 227
 <211> 95
 <212> PRT
 <213> Conus vexillum

<400> 227
 Met Gln Thr Ala Tyr Trp Val Met Val Met Met Met Val Val Gly Phe
 1 5 10 15
 Thr Val Glu Ser His Val His Gln Ser His Ser Pro Thr Ser Arg Ser
 20 25 30
 His Gly Asp Asp Ser Ile His Asp Lys Thr Ile His Gln His Leu Phe
 35 40 45
 Ala Arg Leu Pro Leu Glu Asn Asn Asp Asp His Arg Ser Val Asp Leu
 50 55 60
 Pro Ala Gly Thr Ser Ala Gly Asp Met Lys Pro Gln Arg Gln Lys Arg
 65 70 75 80
 Phe Cys Cys Ile Phe Ala Pro Ile Leu Leu Phe Cys Cys Phe Gly
 85 90 95

<210> 228
 <211> 14
 <212> PRT
 <213> Conus vexillum

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residue 7 may be Pro or hydroxy-Pro

<400> 228
 Phe Cys Cys Ile Phe Ala Xaa Ile Leu Leu Phe Cys Cys Phe
 1 5 10

<210> 229
 <211> 40
 <212> PRT
 <213> Conus tulipa

<400> 229
 Glx Thr Asp Val Leu Leu Glu Ala Thr Leu Leu Thr Thr Pro Ala Pro
 1 5 10 15
 Glu Gln Arg Leu Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg Pro Tyr
 20 25 30
 Pro Trp Arg Arg Arg Asp Leu Asn
 35 40

<210> 230
 <211> 40
 <212> PRT
 <213> Conus magus

<400> 230
 Glx Thr Asp Val Leu Leu Asp Ala Thr Leu Leu Thr Thr Pro Ala Pro
 1 5 10 15

Glu Gln Arg Leu Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg Pro Tyr
20 25 30

Pro Trp Arg Arg Arg Asn Leu Asn
35 40

<210> 231
<211> 40
<212> PRT
<213> Conus geographus

<400> 231
Glx Thr Asp Val Leu Leu Glu Ala Thr Leu Leu Thr Thr Pro Ala Pro
1 5 10 15

Glu Gln Arg Leu Phe Cys Phe Trp Lys Ser Cys Thr Trp Arg Pro Tyr
20 25 30

Pro Trp Arg Arg Arg Asp Leu Asn
35 40

<210> 232
<211> 21
<212> PRT
<213> Conus tulipa

<400> 232
Leu Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg Pro Tyr Pro Trp Arg
1 5 10 15

Arg Arg Asp Leu Asn
20

<210> 233
<211> 21
<212> PRT
<213> Conus magus

<400> 233
Leu Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg Pro Tyr Pro Trp Arg
1 5 10 15

Arg Arg Asn Leu Asn
20

<210> 234
<211> 21
<212> PRT
<213> Conus geographus

<400> 234
Leu Phe Cys Phe Trp Lys Ser Cys Thr Trp Arg Pro Tyr Pro Trp Arg
1 5 10 15

Arg Arg Asp Leu Asn
20

<210> 235
<211> 19
<212> PRT
<213> Conus generalis

<400> 235
Ser His Ser Ser Ser Leu Trp Cys Val Cys Pro Phe Arg Val Cys Pro

1 5 10 15

Pro Cys His

<210> 236
<211> 19
<212> PRT
<213> Conus vexillum

<400> 236
Ser His Ser Ser Ser Leu Trp Cys Val Cys Pro Phe Arg Val Cys Pro
1 5 10 15

Pro Cys His

<210> 237
<211> 33
<212> PRT
<213> Conus flavidus

<400> 237
His Asp His Gly Ile Arg Pro Lys Arg Val Asp Ile Cys Asn Trp Arg
1 5 10 15

Ile Cys Ala Pro Asn Pro Leu Arg Arg His Asp Leu Lys Lys Gly Asn
20 25 30

Asn

<210> 238
<211> 33
<212> PRT
<213> Conus emaciatus

<400> 238
His Thr His Gly Ile Arg Pro Lys Gly Asp Gly Ile Cys Ile Trp Lys
1 5 10 15

Val Cys Pro Pro Asp Pro Trp Arg Arg His Arg Leu Lys Lys Arg Asn
20 25 30

Asn

<210> 239
<211> 33
<212> PRT
<213> Conus aurisiacus

<400> 239
His Thr His Gly Ile Arg Pro Lys Gly Asp Gly Ile Cys Ile Trp Lys
1 5 10 15

Val Cys Pro Pro Asp Pro Trp Arg Arg His His Leu Lys Lys Arg Asn
20 25 30

Asn

<210> 240
<211> 28
<212> PRT
<213> Conus terebra

<400> 240

His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile Trp Lys
 1 5 10 15
 Ile Cys Pro Pro Ser Pro Trp Lys Arg Leu Gly Ser
 20 25

<210> 241
 <211> 28
 <212> PRT
 <213> Conus terebra

<400> 241
 His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile Trp Lys
 1 5 10 15
 Ile Cys Pro Pro Ser Pro Trp Arg Arg Leu Gly Ser
 20 25

<210> 242
 <211> 28
 <212> PRT
 <213> Conus litoglyphus

<400> 242
 His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile Trp Lys
 1 5 10 15
 Ile Cys Pro Pro Ser Pro Trp Lys Arg Arg Leu Gly Ser
 20 25

<210> 243
 <211> 28
 <212> PRT
 <213> Conus litoglyphus

<400> 243
 His Pro His Gly Ile Arg Gln Asp Gly Ala Gln Ile Cys Ile Trp Lys
 1 5 10 15
 Ile Cys Pro Pro Ser Pro Trp Arg Arg Leu Gly Ser
 20 25

<210> 244
 <211> 23
 <212> PRT
 <213> Conus consors

<400> 244
 Asp Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Trp
 1 5 10 15
 Lys Val Cys Pro Pro Ser Pro
 20

<210> 245
 <211> 25
 <212> PRT
 <213> Conus consors

<400> 245
 Asp Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Trp
 1 5 10 15
 Lys Val Cys Pro Pro Ser Pro Trp Lys
 20 25

<210> 246
 <211> 28
 <212> PRT
 <213> Conus consors

<400> 246
 Ala Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Trp
 1 5 10 15
 Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Pro Gln
 20 25

<210> 247
 <211> 26
 <212> PRT
 <213> Conus striolatus

<400> 247
 Ser Asn Thr Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Trp Lys Val
 1 5 10 15
 Cys Pro Pro Ser Pro Trp Arg Arg Ser Gln
 20 25

<210> 248
 <211> 26
 <212> PRT
 <213> Conus striolatus

<400> 248
 Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Asn Trp Lys Val
 1 5 10 15
 Cys Pro Pro Ser Pro Trp Arg Arg Pro Arg
 20 25

<210> 249
 <211> 26
 <212> PRT
 <213> Conus striolatus

<400> 249
 Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile Trp Lys Val
 1 5 10 15
 Cys Pro Pro Ser Pro Trp Arg Arg Ser Gln
 20 25

<210> 250
 <211> 38
 <212> PRT
 <213> Conus striolatus

<400> 250
 Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile Trp Lys Val
 1 5 10 15
 Cys Pro Pro Ser Pro Trp Arg Gln Pro Gln Glu Met Met Asn Asp Ile
 20 25 30
 Arg Gln Pro Pro Gln Leu
 35

<210> 251

<211> 38
 <212> PRT
 <213> Conus striatus

<400> 251
 Ser Asn Asn Gly Arg Ser Ser Gly Ala Gln Ile Cys Ile Trp Lys Val
 1 5 10 15
 Cys Pro Pro Ser Pro Trp Arg Gln Pro Gln Glu Met Met Asn Asp Ile
 20 25 30
 Arg Gln Pro Pro Gln Leu
 35

<210> 252
 <211> 25
 <212> PRT
 <213> Conus aurisiacus

<400> 252
 Leu His Ser Asp Ser Ser Asp Gln Lys Gly Ala Gln Ile Cys Ile Trp
 1 5 10 15
 Lys Val Cys Pro Pro Pro Pro Trp Arg
 20 25

<210> 253
 <211> 34
 <212> PRT
 <213> Conus aurisiacus

<400> 253
 Leu His Ser Asp Ser Ser Asp Gln Lys Gly Gly Met Asn Ala Trp Thr
 1 5 10 15
 Gly Ala Gly Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Pro Pro
 20 25 30

Trp Arg

<210> 254
 <211> 37
 <212> PRT
 <213> Conus aurisiacus

<400> 254
 Leu Arg Ser Asp Ser Ser Asp Gln Lys Gly Gly Met Asn Ala Ser Thr
 1 5 10 15
 Gly Ala Gly Ala Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Ser Pro
 20 25 30

Trp Arg Arg Thr Gln
 35

<210> 255
 <211> 28
 <212> PRT
 <213> Conus circumcisis

<400> 255
 Leu Arg Ser Asp Ser Ser Gly Gln Lys Gly Ala Gln Ile Cys Ile Trp
 1 5 10 15

Lys Val Cys Pro Leu Ser Pro Trp Arg Arg Pro Gln
20 25

<210> 256
<211> 32
<212> PRT
<213> Conus circumciscus

<400> 256
Leu Arg Ser Asp Ser Ser Gly Gln Lys Gly Ala Gln Ile Cys Ile Trp
1 5 10 15

Lys Val Cys Pro Leu Ser Pro Trp Arg Arg Pro Gln Gly Lys Asp Glu
20 25 30

<210> 257
<211> 28
<212> PRT
<213> Conus achatinus

<400> 257
Leu Arg Ser Asp Asn Gly Gly Ser Ser Gly Ala Gln Ile Cys Ile Trp
1 5 10 15

Lys Val Cys Pro Pro Ser Pro Trp Arg Arg Pro Gln
20 25

<210> 258
<211> 22
<212> PRT
<213> Conus stercusmuscarum

<400> 258
Leu Gly Ile Gly Ser Ser Asp Gln Asn Ala Gln Ile Cys Ile Trp Lys
1 5 10 15

Val Cys Pro Pro Ser Pro
20

<210> 259
<211> 25
<212> PRT
<213> Conus consors

<400> 259
Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu Ala Gln Leu Cys Ile Trp
1 5 10 15

Lys Val Cys Pro Pro Ser Pro Trp Arg
20 25

<210> 260
<211> 25
<212> PRT
<213> Conus consors

<400> 260
Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu Ala Gln Leu Cys Ile Trp
1 5 10 15

Lys Val Cys Pro Pro Thr Pro Trp Arg
20 25

<210> 261

<211> 25
 <212> PRT
 <213> Conus magus

<400> 261
 Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu Ala Gln Leu Cys Ile Trp
 1 5 10 15
 Lys Val Cys Pro Pro Ser Pro Trp Arg
 20 25

<210> 262
 <211> 25
 <212> PRT
 <213> Conus nobilis

<400> 262
 Asn Gly Ser Gly Ser Ser Asn Gln Lys Glu Ala Gln Leu Cys Ile Trp
 1 5 10 15
 Lys Val Cys Pro Pro Thr Pro Trp Arg
 20 25

<210> 263
 <211> 27
 <212> PRT
 <213> Conus sulcatus

<400> 263
 Arg Ser Asp Lys Asp Val Gly Lys Arg Met Glu Cys Tyr Trp Lys Ala
 1 5 10 15
 Cys Arg Pro Thr Leu Ser Arg Arg His Asp Leu
 20 25

<210> 264
 <211> 40
 <212> PRT
 <213> Conus bocki

<400> 264
 Arg Ser Asp Lys Asp Asp Pro Gly Gly Gln Glu Cys Tyr Trp Asn Val
 1 5 10 15
 Cys Ala Pro Asn Gln Gly Asp His Met Ile Leu Arg Lys Lys Met Asn
 20 25 30
 Asp Asp Arg Gln Pro Pro Gln Leu
 35 40

<210> 265
 <211> 19
 <212> PRT
 <213> Conus betulinus

<400> 265
 Arg Ser Asp Ser Asp Val Arg Glu Val Pro Val Cys Ser Trp Lys Ile
 1 5 10 15
 Cys Pro Pro

<210> 266
 <211> 22
 <212> PRT

<213> Conus loroisii

<400> 266

Arg Ser Asp Ser Asp Val Arg Glu Val Tyr Ile Leu Cys Ile Trp Lys
1 5 10 15

Ile Cys Pro Pro Leu Pro
20

<210> 267

<211> 32

<212> PRT

<213> Conus gladiator

<400> 267

His Pro Ala Asn Val Arg Gln Gln Gly Lys Ile Cys Val Trp Lys Val
1 5 10 15

Cys Pro Pro Trp Pro Val Arg Ser Pro Gly Pro Gln Pro Lys Asn Lys
20 25 30

<210> 268

<211> 32

<212> PRT

<213> Conus gladiator

<400> 268

His Pro Ala Asn Val Arg Gln Gln Gly Lys Ile Cys Val Trp Lys Val
1 5 10 15

Cys Pro Pro Ser Pro Val Arg Ser Pro Gly Pro Leu Pro Lys Asn Lys
20 25 30

<210> 269

<211> 41

<212> PRT

<213> Conus musicus

<400> 269

Gly Met Gly Pro Gly Asp Leu Ser Leu Gln Lys Met Phe Pro Ser Leu
1 5 10 15

Ala Leu Gly Pro Gly Gly Asp Val Ile Cys Arg Trp Lys Val Cys Pro
20 25 30

Pro Thr Pro Trp Lys Arg Leu Ile Lys
35 40

<210> 270

<211> 49

<212> PRT

<213> Conus musicus

<400> 270

Gly Met Val Pro Gly Asp Leu Ala Leu Gln Tyr Leu Phe Pro Ser Leu
1 5 10 15

Ala Phe Asn Pro Pro Asp Ile Cys Thr Trp Lys Val Cys Pro Pro Pro
20 25 30

Pro Trp Arg Arg Pro Lys Lys Ile Thr Asp Val Gly Gln Pro Pro Gln
35 40 45

Leu

<210> 271
 <211> 49
 <212> PRT
 <213> Conus musicus

<400> 271
 Gly Met Val Pro Gly Asp Leu Val Leu Gln Tyr Leu Phe Pro Ser Leu
 1 5 10 15
 Ala Phe Ser Pro Pro Asp Ile Cys Thr Trp Lys Val Cys Pro Pro Pro
 20 25 30
 Pro Trp Arg Arg Pro Lys Lys Ile Thr Asp Val Arg Gln Pro Pro Gln
 35 40 45

Leu

<210> 272
 <211> 49
 <212> PRT
 <213> Conus musicus

<400> 272
 Gly Met Val Pro Gly Asp Leu Val Leu Gln Tyr Leu Phe Pro Ser Leu
 1 5 10 15
 Ala Phe Asn Pro Pro Asp Ile Cys Thr Trp Lys Val Cys Pro Pro Pro
 20 25 30
 Pro Trp Arg Arg Pro Lys Lys Ile Thr Asp Val Arg Gln Pro Pro Gln
 35 40 45

Leu

<210> 273
 <211> 29
 <212> PRT
 <213> Conus miles

<400> 273
 Glx Gln Asp Gln Ser Pro His His Val Cys Cys Ala Ile Gly Pro Val
 1 5 10 15
 Leu Pro Phe Cys Cys Val Ser Trp Leu His Lys Leu His
 20 25

<210> 274
 <211> 14
 <212> PRT
 <213> Conus miles

<400> 274
 Leu Cys Cys Ile Phe Ala Pro Ile Leu Trp Phe Cys Cys His
 1 5 10

<210> 275
 <211> 13
 <212> PRT
 <213> Conus rattus

<400> 275
 Leu Cys Cys Ile Phe Ala Ile Leu Trp Phe Cys Cys Leu
 1 5 10

<210> 276
 <211> 15
 <212> PRT
 <213> *Conus capitaneus*

<400> 276
 Gly Phe Cys Cys Asp Phe Pro Pro Ile Phe Trp Phe Cys Cys Ile
 1 5 10 15

<210> 277
 <211> 25
 <212> PRT
 <213> *Conus miles*

<400> 277
 Glx Gly Phe Cys Cys Val Val Ile Pro Ile Leu Trp Phe Cys Cys Gly
 1 5 10 15

Gly Tyr Arg Thr Asn Gly Thr Ala Asp
 20 25

<210> 278
 <211> 14
 <212> PRT
 <213> *Conus vexillum*

<400> 278
 Phe Cys Cys Ile Phe Ala Pro Ile Leu Leu Phe Cys Cys Phe
 1 5 10

<210> 279
 <211> 45
 <212> PRT
 <213> *Conus sulcatus*

<400> 279
 Glx Ser Gly Cys Arg Val Pro Phe Glu Leu Lys Cys Ile Trp Lys Phe
 1 5 10 15

Cys Thr Ile Tyr Pro Ser Arg Pro Phe Ala Ser Leu Glu Glu Lys Asp
 20 25 30
 Glu Cys Gln Thr Val Thr Ile Thr Val Thr Trp Asp Phe
 35 40 45

<210> 280
 <211> 45
 <212> PRT
 <213> *Conus cinereus*

<400> 280
 Ser Ser Gly Cys Ser Val Ser Leu Gly Phe Lys Cys Phe Trp Lys Ser
 1 5 10 15

Cys Thr Val Ile Pro Val Arg Pro Phe Val Ser Leu Glu Glu Glu Asn
 20 25 30

Glu Cys Gln Lys Val Gln Ile Ser Ala Val Trp Gly Pro
 35 40 45

<210> 281
 <211> 25
 <212> PRT
 <213> *Conus parius*

<400> 281

Pro Pro Phe Ser Cys Ser Gly Leu Arg Gly Gly Cys Val Leu Pro Pro
 1 5 10 15

Asn Leu Arg Pro Lys Phe Asn Lys Gly
 20 25

<210> 282

<211> 24

<212> PRT

<213> Conus parius

<400> 282

Pro Pro Phe Ser Cys Ala Gly Leu Arg Gly Gly Cys Val Leu Pro Pro
 1 5 10 15

Asn Leu Arg Pro Lys Phe Lys Glu
 20

<210> 283

<211> 29

<212> PRT

<213> Conus wittigi

<400> 283

Ser Ser Asp Gly Ser Asp Pro Lys Ala Lys Lys Gln Cys Met Trp Lys
 1 5 10 15

Arg Cys Ile Pro Asp Gln Ser Arg Leu Glu Glu Asp Glu
 20 25

<210> 284

<211> 30

<212> PRT

<213> Conus cinereus

<400> 284

Ser Ser Asp Gly Lys Ala Lys Lys Gln Cys Ala Trp Lys Thr Cys Val
 1 5 10 15

Pro Thr Gln Trp Arg Arg Arg Asp Leu Lys Glu Lys Asp Glu
 20 25 30

<210> 285

<211> 30

<212> PRT

<213> Conus cinereus

<400> 285

Ser Ser Asp Gly Lys Ala Lys Arg Asn Cys Phe Trp Lys Ala Cys Val
 1 5 10 15

Pro Glu Gln Trp Arg Gln Arg Asp Pro Lys Glu Lys Asp Glu
 20 25 30

<210> 286

<211> 30

<212> PRT

<213> Conus cinereus

<400> 286

Ser Ser Asp Gly Lys Ala Lys Arg Asn Cys Phe Trp Lys Ala Cys Val
 1 5 10 15

Pro Glu Gln Trp Arg Gln Arg Asp Leu Lys Glu Lys Asp Glu
 20 25 30

<210> 287
 <211> 37
 <212> PRT
 <213> Conus nobilis

<400> 287
 Phe Arg Pro Ala Val Lys Ser Arg Ser Arg Arg Ala Pro Pro Cys Val
 1 5 10 15
 Trp Lys Val Cys Pro Ala Pro Pro Trp Leu Val Thr Lys Arg Lys Gln
 20 25 30

Glu Thr Ser Asp Tyr
 35

<210> 288
 <211> 37
 <212> PRT
 <213> Conus nobilis

<400> 288
 Phe Arg Pro Ala Val Lys Ser Arg Ser Arg Arg Ala Pro Pro Cys Val
 1 5 10 15
 Trp Lys Val Cys Pro Ala Pro Pro Trp Leu Val Thr Lys Arg Lys Gln
 20 25 30

Glu Thr Ser Asp Tyr
 35

<210> 289
 <211> 37
 <212> PRT
 <213> Conus miles

<400> 289
 Phe Arg Pro Ala Met Gln Ser Arg Ser Gly Gly Met Ser Leu Cys Leu
 1 5 10 15
 Trp Lys Val Cys Pro Ala Ala Pro Trp Leu Val Ala Lys Arg Lys Gln
 20 25 30

Glu Thr Ser Asp Tyr
 35

<210> 290
 <211> 21
 <212> PRT
 <213> Conus tulipa

<400> 290
 His Phe Asn Ser Val Val Pro Thr Val Tyr Ile Cys Met Trp Lys Val
 1 5 10 15

Cys Pro Pro Ser Pro
 20

<210> 291
 <211> 21
 <212> PRT

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<213> *Conus purpurascens*

<400> 291

Glx Ser Glu Glu Glu Lys Ile Cys Leu Trp Lys Ile Cys Pro Pro Pro
1 5 10 15

Pro Trp Arg Arg Ser
20

<210> 292

<211> 21

<212> PRT

<213> *Conus purpurascens*

<400> 292

Glu Ser Asn Gly Val Glu Ile Cys Met Trp Lys Val Cys Pro Pro Ser
1 5 10 15

Pro Trp Arg Arg Ser
20

<210> 293

<211> 38

<212> PRT

<213> *Conus vexillum*

<400> 293

Ile Met Gln Ser Leu Val Phe Ser His Gln Pro Leu Pro Thr Ala Ser
1 5 10 15

Ile Cys Ile Trp Lys Ile Cys Pro Pro Asp Pro Trp Arg Arg His Asp
20 25 30

Leu Gln Lys Ser Asn Lys
35

<210> 294

<211> 38

<212> PRT

<213> *Conus muriculatus*

<400> 294

Ile Met Gln Ser Leu Val Phe Ser His Gln Pro Leu Pro Thr Ala Ser
1 5 10 15

Ile Cys Ile Trp Lys Ile Cys Pro Pro Asp Pro Trp Arg Arg His Asp
20 25 30

Leu Gln Lys Ser Asn Lys
35

<210> 295

<211> 26

<212> PRT

<213> *Conus pulicarius*

<400> 295

Val Arg Leu Arg Gly Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Leu
1 5 10 15

Leu Gln Trp Ile His Pro Leu Val Lys Arg
20 25

<210> 296

<211> 26
 <212> PRT
 <213> Conus pulicarius

<400> 296
 Val Arg Pro Arg Gly Gln Ile Cys Ile Trp Lys Val Cys Pro Pro Leu
 1 5 10 15
 Leu Gln Trp Ile His Pro Leu Val Lys Arg
 20 25

<210> 297
 <211> 27
 <212> PRT
 <213> Conus pulicarius

<400> 297
 Pro Val Arg Leu Arg Gly Gln Ile Cys Ile Trp Lys Val Cys Pro Pro
 1 5 10 15
 Leu Leu Gln Trp Ile His Pro Leu Val Lys Arg
 20 25

<210> 298
 <211> 30
 <212> PRT
 <213> Conus mustelinus

<400> 298
 Leu Val Ser His Thr Ser Ser Lys Tyr Pro Gly Val Thr Phe Cys Pro
 1 5 10 15
 Trp Lys Val Cys Pro Pro Ala Pro Trp Arg Ile Leu Gly Val
 20 25 30

<210> 299
 <211> 22
 <212> PRT
 <213> Conus baileyi

<400> 299
 His Ser Asp Ser Ile Ile Leu Arg Gly Leu Cys Ile Trp Lys Val Cys
 1 5 10 15
 Glu Pro Pro Pro Gln Arg
 20

<210> 300
 <211> 26
 <212> PRT
 <213> Conus planorbis

<400> 300
 Ser Ser Ser Asn Gly Leu Lys Arg Ala Asp Leu Cys Ile His Lys Ile
 1 5 10 15
 Cys Pro Pro Arg Tyr His Gln Ser Gln Gln
 20 25

<210> 301
 <211> 36
 <212> PRT
 <213> Conus litteratus

<400> 301
 His Arg Val Phe His Leu Asp Asn Thr Tyr Leu Lys Ile Pro Ile Cys
 1 5 10 15
 Ala Trp Lys Val Cys Pro Pro Thr Pro Trp Arg Arg Arg Asp Leu Lys
 20 25 30
 Lys Arg Asn Lys
 35

<210> 302
 <211> 50
 <212> PRT
 <213> Conus litteratus

<400> 302
 Ser Pro Val Ser Thr Pro Tyr Pro Glu Phe His Leu Asp Glu Pro Tyr
 1 5 10 15
 Leu Lys Ile Pro Val Cys Ile Trp Lys Ile Cys Pro Pro Asn Leu Leu
 20 25 30
 Arg Arg Arg Asp Leu Lys Lys Arg Asn Lys Val Arg Gln Thr Thr Ala
 35 40 45

Thr Thr
 50
 <210> 303
 <211> 26
 <212> PRT
 <213> Conus coronatus

<400> 303
 Leu Ser Asp Gly Arg Asp Trp Thr Gly Tyr Ile Cys Ile Trp Lys Ala
 1 5 10 15
 Cys Pro Arg Pro Pro Trp Ile Pro Pro Lys
 20 25

<210> 304
 <211> 29
 <212> PRT
 <213> Conus chaldaeus

<400> 304
 Leu Ser Glu Gly Arg Asn Ser Thr Val His Ile Cys Met Trp Lys Val
 1 5 10 15
 Cys Pro Pro Pro Pro Trp Arg Arg Pro His Gly Gln Arg
 20 25

<210> 305
 <211> 29
 <212> PRT
 <213> Conus chaldaeus

<400> 305
 Leu Ser Glu Gly Arg Asn Ser Thr Val His Ile Cys Thr Trp Lys Val
 1 5 10 15
 Cys Pro Pro Pro Pro Trp Arg Arg Pro His Gly Gln Arg
 20 25

<210> 306

<211> 13
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<400> 306
 Glx Cys Met Trp Lys Arg Cys Ile Pro Asp Gln Ser Arg
 1 5 10

<210> 307
 <211> 15
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<400> 307
 Val Asp Ile Cys Asn Trp Arg Ile Cys Ala Pro Asn Pro Leu Arg
 1 5 10 15

<210> 308
 <211> 13
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa may be Trp (D or L)

<400> 308
 Leu Cys Phe Xaa Lys Ser Cys Arg Pro Tyr Pro Trp Arg
 1 5 10

<210> 309
 <211> 16
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa may be Trp (D or L)

<400> 309
 Leu Phe Cys Phe Xaa Trp Lys Ser Cys Trp Pro Arg Pro Tyr Trp Arg
 1 5 10 15

<210> 310
 <211> 16
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa may be Trp (D or L)

<400> 310
 Leu Phe Cys Phe Xaa Lys Ser Cys Trp Pro Arg Pro Tyr Pro Trp Arg
 1 5 10 15

<210> 311
 <211> 15
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa may be Phe (D or L)

<400> 311
 Leu Xaa Cys Phe Trp Lys Ser Cys Trp Pro Arg Pro Tyr Trp Arg
 1 5 10 15

<210> 312
 <211> 15
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 2 may be Phe (D or L); Xaa at residue 5 may be Trp
 (D or L)

<400> 312
 Leu Xaa Cys Phe Xaa Lys Ser Cys Trp Pro Arg Pro Tyr Trp Arg
 1 5 10 15

<210> 313
 <211> 11
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(11)
 <223> Xaa may be Phe (D or L)

<400> 313
 Leu Xaa Cys Phe Trp Lys Ser Cys Trp Pro Arg
 1 5 10

<210> 314
 <211> 11
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(11)
 <223> Xaa may be Trp (D or L)

<400> 314
 Leu Phe Cys Phe Xaa Lys Ser Cys Trp Pro Arg
 1 5 10

<210> 315
 <211> 11
 <212> PRT
 <213> Conus magus

<220>

<221> PEPTIDE
 <222> (1)..(11)
 <223> Xaa at residue 2 may be Phe (D or L); Xaa at residue 5 may be Trp
 (D or L)

<400> 315
 Leu Xaa Cys Phe Xaa Lys Ser Cys Trp Pro Arg
 1 5 10

<210> 316
 <211> 9
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(9)
 <223> Xaa may be Phe (D or L)
 <400> 316
 Leu Xaa Cys Phe Trp Lys Ser Cys Trp
 1 5

<210> 317
 <211> 9
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(9)
 <223> Xaa may be Trp (D or L)

<400> 317
 Leu Phe Cys Phe Xaa Lys Ser Cys Trp
 1 5

<210> 318
 <211> 9
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(9)
 <223> Xaa at residue 2 may be Phe (D or L); Xaa at residue 5 may be Trp
 (D or L)

<400> 318
 Leu Xaa Cys Phe Xaa Lys Ser Cys Trp
 1 5

<210> 319
 <211> 10
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(10)
 <223> Xaa may be Trp (D or L)

<400> 319
 Phe Cys Phe Xaa Lys Ser Cys Trp Pro Arg
 1 5 10

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<210> 320
 <211> 10
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(10)
 <223> Xaa may be Lys (D or L)

<400> 320
 Phe Cys Phe Trp Xaa Ser Cys Trp Pro Arg
 1 5 10

<210> 321
 <211> 10
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(10)
 <223> Xaa may be Trp (D or L)

<400> 321
 Phe Cys Phe Xaa Phe Ser Cys Trp Pro Arg
 1 5 10

<210> 322
 <211> 10
 <212> PRT
 <213> Conus magus

<400> 322
 Phe Cys Phe Trp Lys Ser Cys Trp Pro Arg
 1 5 10

<210> 323
 <211> 21
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> PEPTIDE
 <222> (1)..(21)
 <223> Xaa may be Trp (D or L)

<400> 323
 Glu Ser Asn Gly Val Glu Ile Cys Met Xaa Lys Val Cys. Pro Pro Ser
 1 5 10 15

Pro Trp Arg Arg Ser
 20

<210> 324
 <211> 14
 <212> PRT
 <213> Conus striatus

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa may be Trp (D or L)

<400> 324
Met Glu Cys Tyr Xaa Lys Ala Cys Arg Pro Thr Leu Ser Arg
1 5 10

<210> 325
<211> 16
<212> PRT
<213> Conus striatus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa may be Trp (D or L)

<400> 325
Phe Glu Leu Lys Cys Ile Xaa Lys Phe Cys Thr Ile Tyr Pro Ser Arg
1 5 10 15

<210> 326
<211> 18
<212> PRT
<213> Conus striatus

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Xaa may be Trp (D or L)

<400> 326
Phe Glu Leu Lys Cys Ile Xaa Lys Phe Cys Thr Ile Tyr Pro Ser Arg
1 5 10 15

Pro Phe

<210> 327
<211> 14
<212> PRT
<213> Conus tulipa

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa may be Trp (D or L)

<400> 327
Thr Val Tyr Ile Cys Met Xaa Lys Val Cys Pro Pro Ser Pro
1 5 10

<210> 328
<211> 22
<212> PRT
<213> Conus aurisiacus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa may be Trp (D or L)

<400> 328
Ser Asp Ser Ser Asp Gln Lys Ala Gln Ile Cys Ile Xaa Lys Val Cys
1 5 10 15

Pro Pro Pro Pro Trp Arg

20

<210> 329
 <211> 16
 <212> PRT
 <213> Conus consors

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa may be Trp (D or L)

<400> 329
 Gly Ala Gln Ile Cys Ile Xaa Lys Val Cys Pro Pro Ser Pro Trp Arg
 1 5 10 15

<210> 330
 <211> 30
 <212> PRT
 <213> Conus musicus

<220>
 <221> PEPTIDE
 <222> (1)..(30)
 <223> Xaa may be Trp (D or L)

<400> 330
 Met Phe Pro Ser Leu Ala Leu Gly Pro Gly Gly Asp Val Ile Cys Arg
 1 5 10 15

Xaa Lys Val Cys Pro Pro Thr Pro Trp Lys Arg Leu Ile Lys
 20 25 30

<210> 331
 <211> 24
 <212> PRT
 <213> Conus flavidus

<220>
 <221> PEPTIDE
 <222> (1)..(24)
 <223> Xaa may be Trp (D or L)

<400> 331
 Val Asp Ile Cys Asn Xaa Arg Ile Cys Ala Pro Asn Pro Leu Arg Arg
 1 5 10 15

His Asp Leu Lys Lys Gly Asn Asn
 20

<210> 332
 <211> 15
 <212> PRT
 <213> Conus flavidus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa may be Trp (D or L)

<400> 332
 Val Asp Ile Cys Asn Xaa Arg Ile Cys Ala Pro Asn Pro Leu Arg
 1 5 10 15

<210> 333
 <211> 22
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa may be Trp (D or L)

<400> 333
 Arg Leu Phe Cys Phe Xaa Lys Ser Cys Thr Trp Arg Pro Tyr Pro Trp
 1 5 10 15

Arg Arg Arg Asp Leu Asn
 20

<210> 334
 <211> 17
 <212> PRT
 <213> Conus generalis

<220>
 <221> DISULFID
 <222> (4)..(14)

<400> 334
 Ser Leu Trp Cys Val Cys Pro Phe Arg Val Cys Pro Pro Cys His Gly
 1 5 10 15

Arg

<210> 335
 <211> 17
 <212> PRT
 <213> Conus generalis

<220>
 <221> DISULFID
 <222> (6)..(14)

<400> 335
 Ser Leu Trp Cys Val Cys Pro Phe Arg Val Cys Pro Pro Cys His Gly
 1 5 10 15

Arg

<210> 336
 <211> 15
 <212> PRT
 <213> Conus generalis

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa may be Phe (D or L)

<220>
 <221> DISULFID
 <222> (4)..(14)

<400> 336
 Ser Leu Trp Cys Val Cys Pro Xaa Arg Val Cys Pro Pro Cys His
 1 5 10 15

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<210> 337
 <211> 15
 <212> PRT
 <213> Conus generalis

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa may be Phe (D or L)

<220>
 <221> DISULFID
 <222> (6)..(14)

<400> 337
 Ser Leu Trp Cys Val Cys Pro Xaa Arg Val Cys Pro Pro Cys His
 1 5 10 15

<210> 338
 <211> 6
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(6)
 <223> Xaa at residues 2 and 5 may be any amino acid; Xaa at residue 3 may be Trp (D or L) or bromo-Trp (D or L)

<400> 338
 Cys Xaa Xaa Lys Xaa Cys
 1 5

<210> 339
 <211> 6
 <212> PRT
 <213> Conus generalis

<220>
 <221> PEPTIDE
 <222> (1)..(6)
 <223> Xaa may be Phe (D or L)

<400> 339
 Cys Pro Xaa Arg Val Cys
 1 5

<210> 340
 <211> 21
 <212> PRT
 <213> Conus ebraeus

<400> 340

Leu Ser Gly Gly Thr Tyr Ser Arg Val Asp Thr Cys Ile Trp Lys Val
 1 5 10 15

Cys Pro Gln Ser Pro
 20

125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999